

OM protein - protein search, using sw model

Run on: August 24, 2004, 14:54:57 ; Search time 69.2687 Seconds
 (without alignments)
 69.343 Million cell updates/sec

Title: US-09-641-801-2
 Perfect score: 89
 Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	89	100.0	17	4	AAB72501	Aab72501 Colostrin
2	89	100.0	17	4	AAB59310	Aab59310 Ewe colos
3	89	100.0	17	4	AAB72247	Aab72247 Colostrin
4	89	100.0	17	4	AAB72533	Aab72533 Colostrin
5	89	100.0	17	5	AAO14578	Aao14578 Neural ce
6	89	100.0	17	5	AAM51037	Aam51037 Colostrin
7	89	100.0	17	5	AAE20229	Aae20229 Colostrin
8	89	100.0	18	4	AAB59341	Aab59341 Ewe colos
9	56	62.9	11	4	AAE07185	Aae07185 Colostrin

10	56	62.9	12	4	AAE07195	Aae07195	Modified
11	48	53.9	692	5	ABP27487	Abp27487	Streptoco
12	48	53.9	692	5	ABP30759	Abp30759	Streptoco
13	48	53.9	692	6	ABU46454	Abu46454	Protein e
14	48	53.9	693	6	ABU44329	Abu44329	Protein e
15	48	53.9	709	5	ABB55615	Abb55615	Lactococc
16	46	51.7	693	2	AAW80722	Aaw80722	S. pneumo
17	46	51.7	693	4	AAU37640	Aau37640	Streptoco
18	46	51.7	693	4	AAM01093	Aam01093	CFE 96 pr
19	46	51.7	693	6	ABU00620	Abu00620	S. pneumo
20	46	51.7	693	6	ABU45840	Abu45840	Protein e
21	45	50.6	83	4	AAM15539	Aam15539	Peptide #
22	45	50.6	83	4	ABB34546	Abb34546	Peptide #
23	45	50.6	83	4	AAM28029	Aam28029	Peptide #
24	45	50.6	83	4	ABB29372	Abb29372	Peptide #
25	45	50.6	83	4	ABB19955	Abb19955	Protein #
26	45	50.6	83	4	AAM67729	Aam67729	Human bon
27	45	50.6	83	4	AAM55332	Aam55332	Human bra
28	45	50.6	83	4	ABG49367	Abg49367	Human liv
29	45	50.6	83	4	AAM03288	Aam03288	Peptide #
30	45	50.6	83	5	ABG37289	Abg37289	Human pep
31	45	50.6	667	2	AAW48760	Aaw48760	BOP1 prot
32	44	49.4	50	6	AAO29916	Aao29916	Human bet
33	44	49.4	133	2	AAV07279	Aay07279	Bovine sy
34	44	49.4	134	2	AAV07278	Aay07278	Human bet
35	43	48.3	417	4	AAG80962	Aag80962	Human nGP
36	43	48.3	417	5	ABG93780	Abg93780	Human G p
37	43	48.3	419	4	AAG80975	Aag80975	Human nGP
38	43	48.3	419	5	ABG93793	Abg93793	Human G p
39	43	48.3	465	6	ABP81710	Abp81710	Human G p
40	43	48.3	466	5	AAE17076	Aae17076	Human G-p
41	43	48.3	466	7	ABW00806	Abw00806	Human GPC
42	43	48.3	468	3	AAB02829	Aab02829	Human G p
43	43	48.3	468	3	AAV71295	Aay71295	Human orp
44	43	48.3	468	6	ABU92263	Abu92263	Human G p
45	43	48.3	470	3	AAV94267	Aay94267	Human G-p

ALIGNMENTS

RESULT 1

AAB72501

ID AAB72501 standard; peptide; 17 AA.

XX

AC AAB72501;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #2.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US022665.
 XX
 PR 17-AUG-1999; 99US-0149310P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2001-218342/22.
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the cell
 PT with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations.
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQGD 17
 |||||
 Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 2

AAB59310

ID AAB59310 standard; peptide; 17 AA.

XX

AC AAB59310;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment A-1.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX
 PR 02-JUN-1999; 99GB-00012852.
 XX
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system and
 PT immune system, viral and bacterial infections, and diseases characterized
 PT by amyloid plaques.
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17
 |||||
 Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 3

AAB72247

ID AAB72247 standard; peptide; 17 AA.

XX

AC AAB72247;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 2.

XX

KW Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX

OS Synthetic.

XX

PN WO200111937-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022818.
 XX
 PR 17-AUG-1999; 99US-0149311P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPPLLQVMMEPQGD 17
 |||||
 Db 1 LQTPQPPLLQVMMEPQGD 17

RESULT 4

AAB72533

ID AAB72533 standard; peptide; 17 AA.

XX

AC AAB72533;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #2.

XX

KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.

XX

OS Unidentified.

XX

PN WO200112651-A2.

XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022774.
XX
PR 17-AUG-1999; 99US-0149633P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
DR WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating damaged
PT neural cells in a patient.
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17
|||||||
Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 5

AAO14578

ID AAO14578 standard; peptide; 17 AA.

XX

AC AAO14578;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 2.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 17

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022777.
 XX
 PR 17-AUG-2000; 2000WO-US022777.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I, Stanton JG, Hughes TK;
 XX
 DR WPI; 2002-269152/31.
 XX
 PT Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 7; Page 21; 37pp; English.
 XX
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQGD 17
 |||||
 Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 6
 AAM51037

ID AAM51037 standard; peptide; 17 AA.
 XX
 AC AAM51037;
 XX
 DT 30-MAY-2002 (first entry)
 XX
 DE Colostrinin constituent peptide.
 XX
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 17
 FT /note= "optional C-terminal amidation"

XX
 PN WO200213849-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022775.
 XX
 PR 17-AUG-2000; 2000WO-US022775.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. Methods are claimed for:
 CC inducing a cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ or an
 CC organism, and the cell is mammalian, including human; modulating an
 CC immune response in a cell by contact with the immunological regulator
 CC under conditions effective to induce a cytokine; modulating an immune
 CC response in a patient by administering an immunological regulator under
 CC conditions effective to induce a cytokine, where the immunological
 CC regulator is administered topically or as part of a dietary supplement,
 CC and where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation by
 CC contacting blood cells with a blood cell regulator, where the blood cells
 CC are present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour
 CC necrosis factor-alpha, interleukin-4, interleukin-6, interleukin-10 and
 CC interleukin-12. It was one of the best overall inducers in almost all
 CC cytokine and blood cell proliferation experiments conducted
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17
 |||||
 Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 7

AAE20229

ID AAE20229 standard; peptide; 17 AA.

XX

AC AAE20229;

XX

DT 18-JUN-2002 (first entry)

XX

DE Colostrinin constituent peptide #2.

XX

KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnerary.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 17

FT /note= "Optionally C-terminal amide"

XX

PN WO200213850-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022776.

XX

PR 17-AUG-2000; 2000WO-US022776.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Stanton GJ, Hughes TK, Boldogh I;

XX

DR WPI; 2002-269151/31.

XX

PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog.

XX

PS Claim 6; Page 25; 51pp; English.

XX

CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress level
CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
CC organ, or organism; or for treating oxidative damage to the skin of a
CC patient e.g. animal or human; to modulate oxidative stress during/ after
CC a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for

CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17
| | | | | | | | | | | | | | |
Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 8

AAB59341

ID AAB59341 standard; peptide; 18 AA.

XX

AC AAB59341;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #1.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to

CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 89; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17

|||||||

Db 2 LQTPQPLLQVMMEPQGD 18

RESULT 9

AAE07185

ID AAE07185 standard; peptide; 11 AA.

XX

AC AAE07185;

XX

DT 06-NOV-2001 (first entry)

XX

DE Colostrinin peptide 1.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;

KW central nervous system disorder; neurodegenerative disorder; weight loss;

KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

KW acquired immunological deficiency; neurological disorder; dementia;

KW antiviral.

XX

OS Unidentified.

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-488775/53.

XX

PT Peptide useful as an interalia in the treatment of e.g. disorders of the

PT immune system and the central nervous system comprises ten amino-terminal

PT amino acid sequence derived from peptides present in colostrinin.

XX

PS Claim 1; Page 15; 40pp; English.

XX

CC The invention relates to colostrinin peptide fragments which are useful,

CC inter alia, in the treatment of chronic disorders of the immune system

CC and the central nervous system. Colostrinin peptides are used as a

CC medicament in the treatment of neurological disorders e.g., dementia,

CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron

CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxillary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child. The
 CC present sequence is colostrinin peptide 1 related to the invention

XX

SQ Sequence 11 AA;

Query Match 62.9%; Score 56; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15

|||||||

Db 1 QPLLQVMMEPQ 11

RESULT 10

AAE07195

ID AAE07195 standard; peptide; 12 AA.

XX

AC AAE07195;

XX

DT 06-NOV-2001 (first entry)

XX

DE Modified colostrinin cyclic peptide #1.

XX

KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;

KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;

KW central nervous system disorder; neurodegenerative disorder; weight loss;

KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

KW acquired immunological deficiency; neurological disorder; dementia;

KW antiviral; cyclic.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic

FT linkage with Gln found at the C-terminal end"

XX

PN WO200155199-A1.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-GB000329.

XX

PR 26-JAN-2000; 2000GB-00001825.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-488775/53.
XX
PT Peptide useful as an interalia in the treatment of e.g. disorders of the
PT immune system and the central nervous system comprises ten amino-terminal
PT amino acid sequence derived from peptides present in colostrinin.
XX
PS Example 2; Page 8; 40pp; English.
XX
CC The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxillary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child. The
CC present sequence is modified colostrinin cyclic peptide #1 related to the
CC invention
XX
SQ Sequence 12 AA;

Query Match 62.9%; Score 56; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQ 15
| | | | | | | | | |
Db 2 QPLLQVMMEPQ 12

RESULT 11

ABP27487

ID ABP27487 standard; protein; 692 AA.

XX

AC ABP27487;

XX

DT 02-JUL-2002 (first entry)

XX

DE Streptococcus polypeptide SEQ ID NO 4150.

XX

KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;

RESULT 12

ABP30759

ID ABP30759 standard; protein; 692 AA.

XX

AC ABP30759;

XX

DT 02-JUL-2002 (first entry)

XX

DE Streptococcus polypeptide SEQ ID NO 10694.

XX

KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial;

KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX

OS Streptococcus agalactiae.

XX

PN WO200234771-A2.

XX

PD 02-MAY-2002.

XX

PF 29-OCT-2001; 2001WO-GB004789.

XX

PR 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.

XX

PA (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX

PI Telford J, Massignani V, Margarit Y RosI, Grandi G, Fraser C;

PI Tettelin H;

XX

DR WPI; 2002-352536/38.

DR N-PSDB; ABN71390.

XX

PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.

XX

PS Claim 1; Page 4179; 4525pp; English.

XX

CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 692 AA;

Query Match 53.9%; Score 48; DB 5; Length 692;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQ 15
:: |:|::|:|:|:
Db 400 IEVPEPVIQLMVEPK 414

RESULT 13

ABU46454

ID ABU46454 standard; protein; 692 AA.

XX

AC ABU46454;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #31981.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Streptococcus pyogenes.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR N-PSDB; ACA50324.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 74378; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 692 AA;

Query Match 53.9%; Score 48; DB 6; Length 692;
 Best Local Similarity 40.0%; Pred. No. 46;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQ 15
 ::|:|::|:|:|:
 Db 400 IEVPEPVIQLMVEPK 414

RESULT 14

ABU44329

ID ABU44329 standard; protein; 693 AA.

XX

AC ABU44329;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #29856.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS *Streptococcus mutans*.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA48199.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 72253; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 693 AA;

Query Match 53.9%; Score 48; DB 6; Length 693;
Best Local Similarity 40.0%; Pred. No. 46;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
::|:|:|:|:|:|:
Db 400 IEVPEPVIQLMVEPK 414

RESULT 15

ABB55615

ID ABB55615 standard; protein; 709 AA.

XX

AC ABB55615;

XX

DT 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

XX

DE Lactococcus lactis protein fusA.

XX

KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.

XX

OS Lactococcus lactis; IL1403.

XX

PN FR2807446-A1.

XX

PD 12-OCT-2001.

XX

PF 11-APR-2000; 2000FR-00004630.

XX

PR 11-APR-2000; 2000FR-00004630.

XX

PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

XX

PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;

XX

DR WPI; 2002-043418/06.

XX

PT New nucleotide sequence useful in the identification or Lactococcus
PT lactis and related species.

XX

PS Claim 6; SEQ ID NO 2317; 2504pp; French.

XX

CC The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic
CC acid sequence is useful in the detection and/or amplification of nucleic
CC acid sequence, particularly to identify Lactococcus lactis or related
CC species. The proteins of the invention are useful for the biosynthesis or
CC biodegradation of a composition of interest. The invention helps research
CC in lactic bacteria, particularly useful in the production of yogurt and
CC cheese. Note: The sequence data for this patent is based on equivalent
CC patent WO200177334 (published 18-OCT-2001) which is available in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)

XX

SQ Sequence 709 AA;

Query Match 53.9%; Score 48; DB 5; Length 709;
Best Local Similarity 40.0%; Pred. No. 47;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
:: |:|::|:|:|:|:
Db 415 IEVPEPVIQLMVEPK 429

Search completed: August 24, 2004, 15:42:11
Job time : 77.2687 secs

OM protein - protein search, using sw model

Run on: August 24, 2004, 15:33:13 ; Search time 18.6493 Seconds
(without alignments)
47.060 Million cell updates/sec

Title: US-09-641-801-2
Perfect score: 89
Sequence: 1 LQTPQPLLQVMMEPQGD 17
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	89	100.0	17	4	US-09-641-803-2	Sequence 2, Appli
2	51	57.3	82	4	US-09-489-039A-11101	Sequence 11101, A
3	45	50.6	667	2	US-08-718-661-2	Sequence 2, Appli
4	41	46.1	99	4	US-09-493-565-2	Sequence 2, Appli
5	41	46.1	294	4	US-09-328-352-7430	Sequence 7430, Ap
6	41	46.1	343	3	US-08-858-003-32	Sequence 32, Appl
7	41	46.1	343	3	US-09-078-166-32	Sequence 32, Appl
8	41	46.1	343	3	US-08-997-467-32	Sequence 32, Appl
9	41	46.1	428	3	US-09-347-833-6	Sequence 6, Appli
10	40.5	45.5	369	2	US-08-596-291-4	Sequence 4, Appli
11	40.5	45.5	369	3	US-09-100-804-4	Sequence 4, Appli

12	40.5	45.5	369	5	PCT-US94-09943-4	Sequence 4, Appli
13	40	44.9	85	4	US-09-621-976-5318	Sequence 5318, Ap
14	40	44.9	671	3	US-09-121-321-16	Sequence 16, Appl
15	40	44.9	671	3	US-08-933-803A-16	Sequence 16, Appl
16	39	43.8	233	4	US-09-328-352-7812	Sequence 7812, Ap
17	39	43.8	319	4	US-09-252-991A-23561	Sequence 23561, A
18	39	43.8	547	4	US-09-855-323-15	Sequence 15, Appl
19	39	43.8	741	4	US-09-252-991A-30333	Sequence 30333, A
20	38.5	43.3	179	4	US-08-858-207A-456	Sequence 456, App
21	38.5	43.3	333	4	US-09-252-991A-31345	Sequence 31345, A
22	38	42.7	76	4	US-09-585-173B-38	Sequence 38, Appl
23	38	42.7	160	4	US-09-489-039A-8491	Sequence 8491, Ap
24	38	42.7	343	4	US-09-489-039A-10892	Sequence 10892, A
25	38	42.7	365	4	US-09-543-681A-6366	Sequence 6366, Ap
26	38	42.7	391	4	US-09-252-991A-24142	Sequence 24142, A
27	38	42.7	436	4	US-09-252-991A-20256	Sequence 20256, A
28	38	42.7	493	4	US-09-489-039A-9811	Sequence 9811, Ap
29	38	42.7	527	4	US-09-489-039A-9695	Sequence 9695, Ap
30	38	42.7	615	4	US-09-134-001C-3284	Sequence 3284, Ap
31	38	42.7	674	4	US-09-252-991A-24934	Sequence 24934, A
32	38	42.7	676	4	US-09-252-991A-24713	Sequence 24713, A
33	38	42.7	711	4	US-09-543-681A-6820	Sequence 6820, Ap
34	38	42.7	822	4	US-09-252-991A-22479	Sequence 22479, A
35	38	42.7	1276	4	US-09-297-937C-13	Sequence 13, Appl
36	38	42.7	1667	4	US-09-489-039A-11624	Sequence 11624, A
37	37.5	42.1	229	4	US-09-252-991A-31789	Sequence 31789, A
38	37.5	42.1	336	4	US-09-252-991A-29624	Sequence 29624, A
39	37.5	42.1	995	4	US-09-362-842-2	Sequence 2, Appli
40	37.5	42.1	2442	4	US-09-514-247A-10	Sequence 10, Appl
41	37	41.6	102	4	US-09-134-001C-5415	Sequence 5415, Ap
42	37	41.6	112	4	US-09-543-681A-5916	Sequence 5916, Ap
43	37	41.6	202	4	US-09-252-991A-22713	Sequence 22713, A
44	37	41.6	204	4	US-09-134-000C-3554	Sequence 3554, Ap
45	37	41.6	328	3	US-09-225-244-2	Sequence 2, Appli

ALIGNMENTS

```

RESULT 1
US-09-641-803-2
; Sequence 2, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-2

Query Match 100.0%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQGD 17
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Db 1 LQTPQPLLQVMMEPQGD 17

RESULT 2

US-09-489-039A-11101
; Sequence 11101, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11101
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11101

Query Match 57.3%; Score 51; DB 4; Length 82;
Best Local Similarity 69.2%; Pred. No. 0.39;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMME 13
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Db 29 LQTPQPLIDAMLE 41

RESULT 3

US-08-718-661-2
; Sequence 2, Application US/08718661
; Patent No. 5876972
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Nucleic acid molecules coding for mammalian
; TITLE OF INVENTION: tumor suppressor proteins and methods for their isolation
; NUMBER OF SEQUENCES: 15

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,661
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 667 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-661-2

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Query Match          50.6%; Score 45; DB 2; Length 667;
Best Local Similarity 60.0%; Pred. No. 35;
Matches      9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 LQTPQPLLQVMMEPQ 15
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Db      543 LPVPQPLPQPMQPMQ 557

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RESULT 4

US-09-493-565-2

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; Sequence 2, Application US/09493565
; Patent No. 6403783
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: No. 6403783ak, Julia E.
; APPLICANT: Raymond, Fenella
; TITLE OF INVENTION: Tumor Marker Zsig62
; FILE REFERENCE: 98-76
; CURRENT APPLICATION NUMBER: US/09/493,565
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-493-565-2

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Query Match          46.1%; Score 41; DB 4; Length 99;
Best Local Similarity 47.1%; Pred. No. 18;
Matches      8; Conservative 5; Mismatches 0; Indels 4; Gaps 1;

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Qy      5 QPLLQ---VMMEPQGD 17
        :|||| :|::|:|
Db      59 RPLLQGCEDIMVQPEGD 75

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RESULT 5

US-09-328-352-7430


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; Sequence 7430, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7430
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7430
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Query Match          46.1%; Score 41; DB 4; Length 294;
Best Local Similarity 37.9%; Pred. No. 60;
Matches 11; Conservative 4; Mismatches 2; Indels 12; Gaps 2;
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Qy      1 LQTPQ-----PLL-----QVMMEPQGD 17
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Db      151 LDTPQDIPILSPLIIEIFYRLLMSPQGD 179
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RESULT 6

US-08-858-003-32

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; Sequence 32, Application US/08858003
; Patent No. 6060234
; GENERAL INFORMATION:
; APPLICANT: Katz, Leonard
; APPLICANT: Stassi, Diane L.
; APPLICANT: Summers Jr., Richard G.
; APPLICANT: Ruan, Xiaoan
; APPLICANT: Pereda-Lopez, Ana
; APPLICANT: Kakavas, Stephan J.
; TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd.
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,003
; FILING DATE: 16-MAY-1979
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne Casuto
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 4952.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847)-938-3137
; TELEFAX: (847)-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6060234e
US-08-858-003-32

```

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Query Match          46.1%; Score 41; DB 3; Length 343;
Best Local Similarity 46.7%; Pred. No. 71;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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Qy      2 QTPQPLLQVMMEPQG 16
        | |:| | |:|
Db      42 QLPRPLKDVLEFAPEG 56

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RESULT 7

US-09-078-166-32

; Sequence 32, Application US/09078166

; Patent No. 6063561

; GENERAL INFORMATION:

; APPLICANT: Katz, Leonard

; APPLICANT: Stassi, Diane L.

; APPLICANT: Summers Jr., Richard G.

; APPLICANT: Ruan, Xiaoan

; APPLICANT: Pereda-Lopez, Ana

; APPLICANT: Kakavas, Stephan J.

; TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES

; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Rd.

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/078,166

; FILING DATE: 16-MAY-1979

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne Casuto
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 4952.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847)-938-3137
; TELEFAX: (847)-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6063561e
US-09-078-166-32

```

```

Query Match          46.1%; Score 41; DB 3; Length 343;
Best Local Similarity 46.7%; Pred. No. 71;
Matches      7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLLQVMMEPQG 16
        | |:|| | : | :|
Db      42 QLPRLKDVLFAPPEG 56

```

RESULT 8

US-08-997-467-32

; Sequence 32, Application US/08997467

; Patent No. 6200813

; GENERAL INFORMATION:

; APPLICANT: Katz, Leonard

; APPLICANT: Stassi, Diane L.

; APPLICANT: Summers Jr., Richard G.

; APPLICANT: Ruan, Xiaoan

; APPLICANT: Pereda-Lopez, Ana

; APPLICANT: Kakavas, Stephan J.

; TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES

; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Rd.

; CITY: Abbott Park

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/997,467
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/858,003
; FILING DATE: 16-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne Casuto
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 4952.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847)-938-3137
; TELEFAX: (847)-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6200813e
US-08-997-467-32

```

```

Query Match          46.1%; Score 41; DB 3; Length 343;
Best Local Similarity 46.7%; Pred. No. 71;
Matches      7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLLQVMMEPQG 16
        | |:|| | : | :|
Db      42 QLPRPLKDVLFAP EG 56

```

RESULT 9

US-09-347-833-6

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; Sequence 6, Application US/09347833
; Patent No. 6294658
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: Factors Involved in Gene Expression
; FILE REFERENCE: BB-1172
; CURRENT APPLICATION NUMBER: US/09/347,833
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,415
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Glycine max
US-09-347-833-6

```

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Query Match          46.1%; Score 41; DB 3; Length 428;
Best Local Similarity 46.7%; Pred. No. 91;
Matches      7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

Qy 2 QTPQPLLQVMMEPQG 16
 | | |::| | |:
Db 273 QQPMPMMQQQMLPRG 287

RESULT 10

US-08-596-291-4

; Sequence 4, Application US/08596291

; Patent No. 5821075

; GENERAL INFORMATION:

; APPLICANT: GONEZ, LEONEL JORGE

; APPLICANT: SARAS, JAN

; APPLICANT: CLAEISSON-WELSH, LENA

; APPLICANT: HELDIN, CARL-HENRIK

; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

; TITLE OF INVENTION: TYROSINE PHOSPHATASES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/596,291

; FILING DATE: 09-AUG-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/115,573

; FILING DATE: 01-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: GATES, EDWARD R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: LO461/7000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; TELEX: 92-1742 EZEKIEL

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-596-291-4

Query Match 45.5%; Score 40.5; DB 2; Length 369;

Best Local Similarity 47.4%; Pred. No. 93;

Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

QY 2 QTP---QPLLQVMMEPQGD 17
:| | | | | : | : |
Db 268 KTPDSAQPLLQLMLDVEED 286

RESULT 11

US-09-100-804-4

; Sequence 4, Application US/09100804

; Patent No. 6066472

; GENERAL INFORMATION:

; APPLICANT: GONEZ, LEONEL JORGE

; APPLICANT: SARAS, JAN

; APPLICANT: CLAESSEON-WELSH, LENA

; APPLICANT: HELDIN, CARL-HENRIK

; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

; TITLE OF INVENTION: TYROSINE PHOSPHATASES

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100,804

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/596,291

; FILING DATE: 09-AUG-1996

; APPLICATION NUMBER: US 08/115,573

; FILING DATE: 01-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/09943

; FILING DATE: 01-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: GATES, EDWARD R.

; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: LO461/7003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-720-3500

; TELEFAX: 617-720-2441

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-100-804-4

Query Match 45.5%; Score 40.5; DB 3; Length 369;
Best Local Similarity 47.4%; Pred. No. 93;
Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

Qy 2 QTP---QPLLQVMMEPQGD 17
:|| |||||:|:: :|
Db 268 KTPDSAQPLLQLMLDVEED 286

RESULT 12

PCT-US94-09943-4

; Sequence 4, Application PC/TUS9409943

; GENERAL INFORMATION:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; APPLICANT:

; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL

; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN

; TITLE OF INVENTION: TYROSINE PHOSPHATASES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; STREET: 600 ATLANTIC AVENUE

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/09943

; FILING DATE: 01-SEP-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/115,573

; FILING DATE: 01-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: TWOMEY, MICHAEL J.

; REGISTRATION NUMBER: P-38,349

; REFERENCE/DOCKET NUMBER: LO461/7000WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/720-3500

; TELEFAX: 617/720-2441

; TELEX: 92-1742 EZEKIEL

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 369 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-09943-4

Query Match 45.5%; Score 40.5; DB 5; Length 369;

Best Local Similarity 47.4%; Pred. No. 93;
Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

Qy 2 QTP---QPLLQVMMEPQGD 17
:| | | | | : | : : |
Db 268 KTPDSAQPLLQLMLDVEED 286

RESULT 13

US-09-621-976-5318
; Sequence 5318, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5318
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -15..-1
US-09-621-976-5318

Query Match 44.9%; Score 40; DB 4; Length 85;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QTPQPLLQV 10
| | | | | | |
Db 59 QPPQPLLQV 67

RESULT 14

US-09-121-321-16
; Sequence 16, Application US/09121321
; Patent No. 6090783
; GENERAL INFORMATION:
; APPLICANT: Saiga, Akihiko
; APPLICANT: Orita, Satoshi
; APPLICANT: Igarashi, Hisanaga
; APPLICANT: Okumura, Kouichi
; APPLICANT: Sakaguchi, Gaku
; TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
; TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York


```

; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,321
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/933,803
; FILING DATE: 19-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-12CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-121-321-16

```

```

Query Match          44.9%; Score 40; DB 3; Length 671;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches      8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLLQVMMEPQ 15
        | ||| || :||
Db      415 QPPQPQLQSQPQPQ 428

```

RESULT 15

US-08-933-803A-16

```

; Sequence 16, Application US/08933803A
; Patent No. 6218522

```

GENERAL INFORMATION:

```

; APPLICANT: Saiga, Akihiko
; APPLICANT: Orita, Satoshi
; APPLICANT: Igarashi, Hisanaga
; APPLICANT: Okumura, Kouichi
; APPLICANT: Sakaguchi, Gaku
; TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
; TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,803A
; FILING DATE: 19-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley, James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-12CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 671 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-933-803A-16

```

```

Query Match          44.9%; Score 40; DB 3; Length 671;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches      8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLLQVMMEPQ 15
        | ||| || :||
Db      415 QPPQPQLQSQPQPQ 428

```

```

Search completed: August 24, 2004, 15:55:11
Job time : 19.6493 secs

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OM protein - protein search, using sw model

Run on: August 24, 2004, 15:26:28 ; Search time 16.4925 Seconds
 (without alignments)
 99.151 Million cell updates/sec

Title: US-09-641-801-2
 Perfect score: 89
 Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	53.9	709	2	D86907	elongation factor
2	47.5	53.4	192	2	AF1753	Orf50 [bacterioph
3	46	51.7	639	2	S03268	tetracycline resis
4	46	51.7	693	2	B95032	translation elonga
5	46	51.7	693	2	B97903	elongation factor
6	44	49.4	134	2	S44430	synuclein - human
7	44	49.4	134	2	S39046	phosphoneuroprotei
8	44	49.4	137	2	I56498	phosphoneuroprotei
9	44	49.4	671	2	C96534	probable Poly-A Bi
10	43	48.3	134	2	AB0784	conserved hypothet
11	43	48.3	639	2	S13142	tetracycline resis
12	43	48.3	639	2	A60633	tetracycline resis
13	43	48.3	639	2	A56779	tetracycline resis

14	43	48.3	695	2	AE1406	translation elonga
15	43	48.3	695	2	AE1782	translation elonga
16	43	48.3	699	2	AC2816	translation elonga
17	43	48.3	699	2	E97594	elongation factor
18	43	48.3	844	2	F86231	hypothetical prote
19	42	47.2	263	2	S74353	carbonic anhydrase
20	42	47.2	580	2	S13328	hypothetical prote
21	42	47.2	595	2	F85438	nucleoporin-like p
22	42	47.2	643	2	S55610	polyprotein - equi
23	42	47.2	698	2	C82332	translation elonga
24	41	46.1	78	2	D91160	hypothetical prote
25	41	46.1	78	2	C86006	hypothetical prote
26	41	46.1	78	2	E65136	hypothetical 8.7 k
27	41	46.1	639	2	A24333	tetracycline resis
28	41	46.1	641	2	JN0800	tetracycline-minoc
29	41	46.1	857	2	JC4169	phosphoenolpyruvat
30	41	46.1	1058	1	WMBE52	UL52 protein - hum
31	41	46.1	1653	2	B91052	hypothetical prote
32	41	46.1	1653	2	F85896	hypothetical prote
33	41	46.1	1653	2	G65028	hypothetical prote
34	40.5	45.5	549	2	S53427	protein-tyrosine-p
35	40.5	45.5	656	1	A55574	protein-tyrosine-p
36	40.5	45.5	656	1	JC4263	protein-tyrosine-p
37	40	44.9	237	2	G72676	hypothetical prote
38	40	44.9	259	2	T14439	hypothetical prote
39	40	44.9	282	2	T14440	hypothetical prote
40	40	44.9	284	2	T47277	lactoylglutathione
41	40	44.9	300	2	T21149	hypothetical prote
42	40	44.9	357	2	E96696	protein FlN21.10 [
43	40	44.9	357	2	T38405	hypothetical prote
44	40	44.9	380	2	H87344	esterase, probable
45	40	44.9	691	1	EFTWG	translation elonga

ALIGNMENTS

RESULT 1

D86907

elongation factor G [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)

C;Species: *Lactococcus lactis* subsp. *lactis*

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: D86907

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.D.; Sorokin, A.

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. *lactis* IL1403.

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: D86907

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-709 <STO>

A;Cross-references: GB:AE005176; PID:g12725331; PIDN:AAK06358.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

C;Superfamily: translation elongation factor G; translation elongation factor Tu
homology

```
Qy      1  LQTPQPLLQVMMEPQ 15
          :: ||::||::||:
Db     415  IEVPEPVIQLMVEPK 429
```

A; Gene: lin2571

```

Qy      3 TPQPL---LQVMMEPQGD 17
      ||::||  :::::| |||||
Db     31 TPKPLPGGVEISVEPQGD 48

```

C;Accession: S03268

R;Sanchez-Pescador, R.; Brown, J.T.; Roberts, M.; Urdea, M.S.
 Nucleic Acids Res. 16, 1216-1217, 1988
 A;Title: The nucleotide sequence of the tetracycline resistance determinant tetM
 from Ureaplasma urealyticum.
 A;Reference number: S03268; MUID:88144009; PMID:3344217
 A;Accession: S03268
 A;Molecule type: DNA
 A;Residues: 1-639 <SAN>
 A;Cross-references: GB:U08812; EMBL:X06901; NID:g475983; PIDN:AAA73978.1;
 PID:g475984
 C;Genetics:
 A;Gene: tetM
 A;Genetic code: SGC3
 C;Superfamily: translation elongation factor G; translation elongation factor Tu
 homology
 C;Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop
 F;4-131/Domain: translation elongation factor Tu homology <ETU>
 F;10-17/Region: nucleotide-binding motif A (P-loop)
 F;128-131/Region: GTP-binding NKXD motif
 F;220-222/Region: GTP-binding SAK/L motif
 F;16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp,
 Ser) #status predicted

Query Match	51.7%;	Score 46;	DB 2;	Length 639;
Best Local Similarity	50.0%;	Pred. No. 11;		
Matches	7;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
 :: | ||||: :||
 Db 339 IENPHPLLQITVEP 352

RESULT 4

B95032
 translation elongation factor G [imported] - Streptococcus pneumoniae (strain
 TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
 C;Accession: B95032
 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson,
 S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn,
 M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.;
 Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.;
 Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.;
 Dickinson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.;
 Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus
 pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: B95032
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-693 <KUR>
 A;Cross-references: GB:AE005672; PIDN:AAK74451.1; PID:g14971744; GSPDB:GN00164;
 TIGR:SP4SP0273

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0273

C;Superfamily: translation elongation factor G; translation elongation factor Tu
homology

Query Match 51.7%; Score 46; DB 2; Length 693;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
: |:|::|:|:|:
Db 400 INVPEPVIQLMVEPK 414

RESULT 5

B97903

elongation factor G [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

C;Accession: B97903

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff,
B.S.; Estrem, S.; Fritz, L.; Fu, D.J.; Fuller, W.; Geringer, C.; Gilmour, R.;
Glass, J.S.; Khoja, H.; Kraft, A.; LaGace, R.; LeBlanc, D.J.; Lee, L.N.;
Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; McHenney, M.; McLeaster,
K.; Mundy, C.; Nicas, T.I.; Norris, F.H.; O'Gara, M.; Peery, R.; Robertson,
G.T.; Rockey, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.;
Jaskunas, S.R.; Rosteck Jr., P.R.; Skatrud, P.L.; Glass, J.I.

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: B97903

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-693 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAK99054.1; PID:g15457799; GSPDB:GN00174

C;Genetics:

A;Gene: fusA

C;Superfamily: translation elongation factor G; translation elongation factor Tu
homology

Query Match 51.7%; Score 46; DB 2; Length 693;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
: |:|::|:|:|:
Db 400 INVPEPVIQLMVEPK 414

RESULT 6

S44430

synuclein - human

C;Species: Homo sapiens (man)

C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 28-May-1999

C;Accession: S44430

R;Jakes, R.; Spillantini, M.G.; Goedert, M.
FEBS Lett. 345, 27-32, 1994
A;Title: Identification of two distinct synucleins from human brain.
A;Reference number: S44430; MUID:94252398; PMID:8194594
A;Accession: S44430
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <JAK>
A;Cross-references: GB:S69965; NID:g546911; PIDN:AAB30860.1; PID:g546912

Query Match 49.4%; Score 44; DB 2; Length 134;
Best Local Similarity 46.2%; Pred. No. 3.9;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
:|:::|::|:
Db 105 EPLIEPLMEPEGE 117

RESULT 7

S39046

phosphoneuroprotein 14 - bovine

N;Alternate names: brain-specific protein, 14K

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-May-1994 #sequence_revision 05-May-1995 #text_change 05-May-1995

C;Accession: S39046; JU0238

R;Nakajo, S.; Tsukada, K.; Omata, K.; Nakamura, Y.; Nakaya, K.

Eur. J. Biochem. 217, 1057-1063, 1993

A;Title: A new brain-specific 14-kDa protein is a phosphoprotein. Its complete amino acid sequence and evidence for phosphorylation.

A;Reference number: S39046; MUID:94039126; PMID:8223629

A;Accession: S39046

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-134 <NAK>

R;Nakajo, S.; Tsukada, K.; Omata, K.; Nakamura, Y.; Nakaya, K.

submitted to JIPID, October 1993

A;Description: A new brain-specific 14-kDa protein is a phosphoprotein: Its complete amino acid sequence and evidence for phosphorylation.

A;Reference number: JU0238

A;Accession: JU0238

A;Molecule type: protein

A;Residues: 1-134 <NA2>

C;Keywords: brain

Query Match 49.4%; Score 44; DB 2; Length 134;
Best Local Similarity 46.2%; Pred. No. 3.9;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
:|:::|::|:
Db 105 EPLIEPLMEPEGE 117

RESULT 8

I56498

phosphoneuroprotein 14 - rat

C;Species: Rattus sp. (rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I56498
 R;Tobe, T.; Nakajo, S.; Tanaka, A.; Mitoya, A.; Omata, K.; Nakaya, K.; Tomita, M.; Nakamura, Y.
 J. Neurochem. 59, 1624-1629, 1992
 A;Title: Cloning and characterization of the cDNA encoding a novel brain-specific 14-kDa protein.
 A;Reference number: I56498; MUID:93019240; PMID:1402909
 A;Accession: I56498
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-137 <RES>
 A;Cross-references: GB:D17764; NID:g409780; PIDN:BAA04610.1; PID:g459235

Query Match 49.4%; Score 44; DB 2; Length 137;
 Best Local Similarity 46.2%; Pred. No. 4;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
 :||:::||:|:
 Db 105 EPLIEPLMEPEGE 117

RESULT 9

C96534

probable Poly-A Binding Protein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C;Accession: C96534

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.; Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: C96534

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-671 <STO>

A;Cross-references: GB:AE005173; NID:g10120431; PIDN:AAG13056.1; GSPDB:GN00141

C;Genetics:

A;Gene: F14J22.3

A;Map position: 1

C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 49.4%; Score 44; DB 2; Length 671;
Best Local Similarity 46.7%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEPQG 16
| | |::| | |:
Db 514 QQPSPMMQQQMHPRG 528

RESULT 10

AB0784

conserved hypothetical protein STY2446 [imported] - *Salmonella enterica* subsp. *enterica* serovar Typhi (strain CT18)

C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A;Note: this species has also been called *Salmonella typhi*

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AB0784

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.

A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi CT18.

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB0784

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-134 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD02592.1; PID:g16503449; GSPDB:GN00176

C;Genetics:

A;Gene: STY2446

Query Match 48.3%; Score 43; DB 2; Length 134;
Best Local Similarity 61.5%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEP 14
| |||| | |:
Db 63 QAPQPLRQSMLSP 75

RESULT 11

S13142

tetracycline resistance protein tetM - *Enterococcus faecalis* transposon Tn916

C;Species: *Enterococcus faecalis*

C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 02-Feb-2001

C;Accession: S13142

R;Burdett, V.

Nucleic Acids Res. 18, 6137, 1990

A;Title: Nucleotide sequence of the tet(M) gene of Tn916.

A;Reference number: S13142; MUID:91045089; PMID:2172929
 A;Accession: S13142
 A;Molecule type: DNA
 A;Residues: 1-639 <BUR>
 A;Cross-references: EMBL:X56353; NID:g47061; PIDN:CAA39796.1; PID:g47062
 R;Burdett, V.
 J. Biol. Chem. 266, 2872-2877, 1991
 A;Title: Purification and characterization of Tet(M), a protein that renders ribosomes resistant to tetracycline.
 A;Reference number: A23749; MUID:91131580; PMID:1993661
 A;Contents: annotation; function; amino end of purified recombinant protein
 A;Note: protein purified after expression in E. coli shown to be ribosome-dependent GTPase
 C;Genetics:
 A;Gene: tetM
 C;Superfamily: translation elongation factor G; translation elongation factor Tu homology
 C;Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop
 F;4-131/Domain: translation elongation factor Tu homology <ETU>
 F;10-17/Region: nucleotide-binding motif A (P-loop)
 F;128-131/Region: GTP-binding NKXD motif
 F;220-222/Region: GTP-binding SAK/L motif
 F;16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #status predicted

Query Match	48.3%;	Score 43;	DB 2;	Length 639;
Best Local Similarity	50.0%;	Pred. No. 34;		
Matches	7;	Conservative	3;	Mismatches 4; Indels 0; Gaps 0;

Qy	1	LQTPQPLLQVMMEP	14
		:: :	
Db	339	IENPHPLLQTTVEP	352

RESULT 12

A60633

tetracycline resistance protein - *Staphylococcus aureus* (strain MRSA101)

C;Species: *Staphylococcus aureus*

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 02-Feb-2001

C;Accession: A60633

R;Nesin, M.; Svec, P.; Lupski, J.R.; Godson, G.N.; Kreiswirth, B.; Kornblum, J.; Projan, S.J.

Antimicrob. Agents Chemother. 34, 2273-2276, 1990

A;Title: Cloning and nucleotide sequence of a chromosomally encoded tetracycline resistance determinant, tetA(M), from a pathogenic, methicillin-resistant strain of *Staphylococcus aureus*.

A;Reference number: A60633; MUID:91158314; PMID:2073121

A;Accession: A60633

A;Molecule type: DNA

A;Residues: 1-639 <NES>

A;Cross-references: GB:M21136; NID:g153114; PIDN:AAA26678.1; PID:g153115

C;Superfamily: translation elongation factor G; translation elongation factor Tu homology

C;Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop

F;4-131/Domain: translation elongation factor Tu homology <ETU>

F;10-17/Region: nucleotide-binding motif A (P-loop)

F;128-131/Region: GTP-binding NKXD motif

F;220-222/Region: GTP-binding SAK/L motif
F;16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 639;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | |||| :||
Db 339 IENPHPLLQTTVEP 352

RESULT 13

A56779

tetracycline resistance protein TetM - Enterococcus faecalis transposon Tn916

C;Species: Enterococcus faecalis

C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 02-Feb-2001

C;Accession: A56779

R;Su, Y.A.; He, P.; Clewell, D.B.

Antimicrob. Agents Chemother. 36, 769-778, 1992

A;Title: Characterization of the tet(M) determinant of Tn916: evidence for regulation by transcription attenuation.

A;Reference number: A56779; MUID:92368175; PMID:1323953

A;Accession: A56779

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-639 <SU1>

A;Cross-references: GB:M85225; NID:g148321; PIDN:AAA24784.1; PID:g148322

A;Note: sequence extracted from NCBI backbone (NCBIN:111076, NCBIP:111078)

C;Superfamily: translation elongation factor G; translation elongation factor Tu homology

C;Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop

F;4-131/Domain: translation elongation factor Tu homology <ETU>

F;10-17/Region: nucleotide-binding motif A (P-loop)

F;128-131/Region: GTP-binding NKXD motif

F;220-222/Region: GTP-binding SAK/L motif

F;16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 639;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | |||| :||
Db 339 IENPHPLLQTTVEP 352

RESULT 14

AE1406

translation elongation factor G homolog fus [imported] - Listeria monocytogenes (strain EGD-e)

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C;Accession: AE1406

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.; Jackson, D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Remmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P.
 A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AE1406
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-695 <GLA>
 A;Cross-references: GB:NC_003210; PIDN:CAD00867.1; PID:g16412154; GSPDB:GN00177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: fus
 C;Superfamily: translation elongation factor G; translation elongation factor Tu homology

Query Match	48.3%;	Score 43;	DB 2;	Length 695;
Best Local Similarity	40.0%;	Pred. No. 38;		
Matches	6;	Conservative	7;	Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
 :: |:|::|| :||:
 Db 399 MEFPEPVIQVAIEPK 413

RESULT 15

AE1782
 translation elongation factor G homolog fus [imported] - *Listeria innocua* (strain Clip11262)
 C;Species: *Listeria innocua*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
 C;Accession: AE1782
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakraborty, T.; Charbit, A.; Chetouani, F.; Couve, E.; de Daruvar, A.; Dehoux, P.; Domann, E.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Garcia-Del Portillo, F.; Garrido, P.; Gautier, L.; Goebel, W.; Gomez-Lopez, N.; Hain, T.; Hauf, J.; Jackson, D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mata Vicente, J.; Ng, E.; Nordsiek, G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Remmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, J.; Cossart, P.
 A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AE1782
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-695 <GLA>

A;Cross-references: GB:AL592022; PIDN:CAC98029.1; PID:g16415339; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: fus
C;Superfamily: translation elongation factor G; translation elongation factor Tu
homology

Query Match 48.3%; Score 43; DB 2; Length 695;
Best Local Similarity 40.0%; Pred. No. 38;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
:: |:|:|:|:|:|:
Db 399 MEFPEPVIQVAIEPK 413

Search completed: August 24, 2004, 15:52:41
Job time : 19.4925 secs

OM protein - protein search, using sw model

Run on: August 24, 2004, 15:51:19 ; Search time 61.5299 Seconds
(without alignments)
86.825 Million cell updates/sec

Title: US-09-641-801-2
Perfect score: 89
Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				ID	Description
No.	Score	Match	Length	DB			

1	89	100.0	17	14	US-10-281-652-2	Sequence 2, Appli
2	48	53.9	692	12	US-10-282-122A-74378	Sequence 74378, A
3	48	53.9	693	12	US-10-282-122A-72253	Sequence 72253, A
4	46	51.7	693	9	US-09-815-242-13233	Sequence 13233, A
5	46	51.7	693	12	US-10-282-122A-73764	Sequence 73764, A
6	45	50.6	83	9	US-09-864-761-35253	Sequence 35253, A
7	44	49.4	50	14	US-10-223-978-2	Sequence 2, Appli
8	44	49.4	549	12	US-10-425-114-51657	Sequence 51657, A
9	43	48.3	296	9	US-09-789-054A-10	Sequence 10, Appl
10	43	48.3	296	15	US-10-374-780A-824	Sequence 824, App
11	43	48.3	296	16	US-10-437-963-126258	Sequence 126258,
12	43	48.3	417	10	US-09-782-974C-68	Sequence 68, Appl
13	43	48.3	419	10	US-09-782-974C-94	Sequence 94, Appl
14	43	48.3	465	14	US-10-225-567A-595	Sequence 595, App
15	43	48.3	466	14	US-10-079-384-10	Sequence 10, Appl
16	43	48.3	468	12	US-09-875-076-10	Sequence 10, Appl
17	43	48.3	468	12	US-09-876-252-10	Sequence 10, Appl
18	43	48.3	468	14	US-10-272-983-10	Sequence 10, Appl
19	43	48.3	468	14	US-10-393-807-10	Sequence 10, Appl
20	43	48.3	468	15	US-10-417-820A-10	Sequence 10, Appl
21	43	48.3	468	16	US-10-723-955-10	Sequence 10, Appl
22	43	48.3	468	16	US-10-782-596-10	Sequence 10, Appl
23	43	48.3	470	9	US-09-805-467A-2	Sequence 2, Appli
24	43	48.3	470	12	US-10-343-650A-10	Sequence 10, Appl
25	43	48.3	470	13	US-10-006-950-2	Sequence 2, Appli
26	43	48.3	470	14	US-10-219-113-2	Sequence 2, Appli
27	43	48.3	470	14	US-10-017-161-1058	Sequence 1058, Ap
28	43	48.3	470	15	US-10-292-798-900	Sequence 900, App
29	43	48.3	505	10	US-09-782-974C-92	Sequence 92, Appl
30	43	48.3	631	12	US-10-282-122A-57461	Sequence 57461, A
31	43	48.3	695	12	US-10-282-122A-61020	Sequence 61020, A
32	43	48.3	844	12	US-10-225-066A-804	Sequence 804, App
33	43	48.3	844	15	US-10-374-780A-2260	Sequence 2260, Ap
34	42	47.2	92	9	US-09-738-626-3898	Sequence 3898, Ap
35	42	47.2	325	14	US-10-032-585-7089	Sequence 7089, Ap
36	42	47.2	344	12	US-10-424-599-217815	Sequence 217815,
37	42	47.2	698	12	US-10-282-122A-77020	Sequence 77020, A
38	42	47.2	1451	16	US-10-437-963-126086	Sequence 126086,
39	42	47.2	2479	16	US-10-437-963-126085	Sequence 126085,
40	41	46.1	38	14	US-10-315-964A-5	Sequence 5, Appli
41	41	46.1	38	14	US-10-317-251A-5	Sequence 5, Appli
42	41	46.1	38	14	US-10-317-252A-5	Sequence 5, Appli
43	41	46.1	85	12	US-10-425-114-44285	Sequence 44285, A
44	41	46.1	99	13	US-10-058-580-2	Sequence 2, Appli
45	41	46.1	141	12	US-10-424-599-256478	Sequence 256478,

ALIGNMENTS

RESULT 1

US-10-281-652-2

; Sequence 2, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John


```
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-2
```

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Query Match          100.0%; Score 89; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 LQTPQPLLQVMMEPQGD 17
          |||||
Db      1 LQTPQPLLQVMMEPQGD 17
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RESULT 2

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US-10-282-122A-74378
; Sequence 74378, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
```



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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72253
;   LENGTH: 693
;   TYPE: PRT
;   ORGANISM: Streptococcus mutans
US-10-282-122A-72253

```

```

Query Match          53.9%;   Score 48;   DB 12;   Length 693;
Best Local Similarity 40.0%;   Pred. No. 63;
Matches      6;   Conservative      8;   Mismatches      1;   Indels      0;   Gaps      0;

```

```

Qy      1 LQTPQPLLQVMMEPQ 15
      :: |:|::|:|:|:|:|:
Db      400 IEVPEPVIQLMVEPK 414

```

```

RESULT 4
US-09-815-242-13233
; Sequence 13233, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23

```

; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13233
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13233

Query Match 51.7%; Score 46; DB 9; Length 693;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
: |:|::|:|:|:
Db 400 INVPEPVIQLMVEPK 414

RESULT 5

US-10-282-122A-73764
; Sequence 73764, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347

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; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73764
;   LENGTH: 693
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-10-282-122A-73764
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Query Match          51.7%;   Score 46;   DB 12;   Length 693;
Best Local Similarity 40.0%;   Pred. No. 1.3e+02;
Matches      6;   Conservative      7;   Mismatches      2;   Indels      0;   Gaps      0;
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Qy          1 LQTPQPLLQVMMEPQ 15
              : |:|::|:|:|:|:
Db          400 INVPEPVIQLMVEPK 414
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RESULT 6

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US-09-864-761-35253
; Sequence 35253, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35253
;   LENGTH: 83
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AP000352.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.1
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.8
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.7
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.9
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.8
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.7
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 8.5
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.4
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6
;   OTHER INFORMATION: EST_HUMAN HIT: AA931620.1, EVALUE 3.70e-02
;   OTHER INFORMATION: SWISSPROT HIT: P09279, EVALUE 1.60e+00
US-09-864-761-35253

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Query Match          50.6%;  Score 45;  DB 9;  Length 83;
Best Local Similarity 60.0%;  Pred. No. 19;
Matches      9;  Conservative 1;  Mismatches 5;  Indels 0;  Gaps 0;

```

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Qy      1 LQTPQPLLQVMMEPQ 15
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Db      21 LQKPQPLLASLASEPQ 35

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RESULT 7
US-10-223-978-2
; Sequence 2, Application US/10223978

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; Publication No. US20030125522A1
; GENERAL INFORMATION:
; APPLICANT: Atgen Co., Ltd.
; APPLICANT: Kim, Jong-Sun
; TITLE OF INVENTION: No. US20030125522A1e1 Peptides Conferring Environmental Stress Resistance And Fusion
; TITLE OF INVENTION: Proteins Including Said Peptides
; FILE REFERENCE: 59520-00003
; CURRENT APPLICATION NUMBER: US/10/223,978
; CURRENT FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(50)
; OTHER INFORMATION: Acidic tail amino acid sequence 85-134 of beta-synuclein
US-10-223-978-2

Query Match 49.4%; Score 44; DB 14; Length 50;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
:|:::|::|:
Db 21 EPLIEPLMEPEGE 33

RESULT 8

US-10-425-114-51657
; Sequence 51657, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51657
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-095-C11_FLI.pep
US-10-425-114-51657

Query Match 49.4%; Score 44; DB 12; Length 549;
Best Local Similarity 56.2%; Pred. No. 2e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQG 16
|: ||||| | : ||
Db 324 LRYPQPLLsvAVSPCG 339

RESULT 9

US-09-789-054A-10

; Sequence 10, Application US/09789054A
; Publication No. US20020184659A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: PLANT GENES ENCODING DR1 AND DRAP1, A GLOBAL REPRESSOR
COMPLEX OF
; TITLE OF INVENTION: TRANSCRIPTION
; FILE REFERENCE: BB1107 US CIP
; CURRENT APPLICATION NUMBER: US/09/789,054A
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/485558
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US98/16688
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: 60/055,865
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 10
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-789-054A-10

Query Match 48.3%; Score 43; DB 9; Length 296;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEPQ 15
||||| || :||
Db 199 QTPQPQPQVHPQPQ 212

RESULT 10

US-10-374-780A-824

; Sequence 824, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver


```

; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 824
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G484
US-10-374-780A-824

```

```

Query Match          48.3%; Score 43; DB 15; Length 296;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches      9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy      2 QTPQPLLQVMMEPQ 15
        |||||  ||  :||
Db      199 QTPQPQPQVHPQPQ 212

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RESULT 11
US-10-437-963-126258
; Sequence 126258, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```

```

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126258
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_28822C.1.pep
US-10-437-963-126258

```

```

Query Match          48.3%; Score 43; DB 16; Length 296;
Best Local Similarity 64.3%; Pred. No. 1.5e+02;
Matches      9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      2 QTPQPLLQVMMEPQ 15
        |||||  ||  :||
Db      199 QTPQPQPQVHPQPQ 212

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RESULT 12

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US-09-782-974C-68
; Sequence 68, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421

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; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-68

Query Match 48.3%; Score 43; DB 10; Length 417;
Best Local Similarity 53.3%; Pred. No. 2.2e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 TPQPLLQVMMEPQGD 17
| || | : | : || |
Db 385 TAQPQLNLMAQPQSD 399

RESULT 13

US-09-782-974C-94

; Sequence 94, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-94

Query Match 48.3%; Score 43; DB 10; Length 419;
Best Local Similarity 53.3%; Pred. No. 2.2e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEPQGD 17
| || | : | : || |
Db 387 TAQPQLNLMAQPQSD 401

RESULT 14

US-10-225-567A-595

; Sequence 595, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 595
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-595

Query Match 48.3%; Score 43; DB 14; Length 465;
Best Local Similarity 53.3%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEPQGD 17
| || | : | : || |
Db 383 TAQPQLNLMAQPQSD 397

RESULT 15

US-10-079-384-10

; Sequence 10, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier

; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED
RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-10

Query Match 48.3%; Score 43; DB 14; Length 466;
Best Local Similarity 53.3%; Pred. No. 2.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TPQPLLQVMMEPQGD 17
| | | | : | : | |
Db 383 TAQPQLNLMAQPQSD 397

Search completed: August 24, 2004, 16:41:13
Job time : 63.5299 secs

OM protein - protein search, using sw model

Run on: August 24, 2004, 15:23:00 ; Search time 52.5224 Seconds
(without alignments)
102.124 Million cell updates/sec

Title: US-09-641-801-2
Perfect score: 89
Sequence: 1 LQTPQPLLQVMMPEQGD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : SPTREMBL_25:*
1:  sp_archea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
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1	47.5	53.4	192	16	Q928G4	Q928g4 listeria in
2	46	51.7	473	2	Q84GV8	Q84gv8 lactobacill
3	46	51.7	473	2	Q84GV7	Q84gv7 lactobacill
4	46	51.7	474	2	Q84GW2	Q84gw2 lactobacill
5	46	51.7	474	2	Q84GV1	Q84gv1 lactobacill
6	46	51.7	475	2	Q84GW0	Q84gw0 lactobacill
7	46	51.7	475	2	Q84GU9	Q84gu9 lactobacill
8	46	51.7	477	2	Q84GW4	Q84gw4 lactobacill
9	46	51.7	477	2	Q84GW3	Q84gw3 lactobacill
10	46	51.7	484	2	Q84GU5	Q84gu5 lactobacill
11	45	50.6	667	11	O35745	O35745 mus musculu
12	45	50.6	675	11	Q9EPT3	Q9ept3 mus musculu
13	45	50.6	704	11	Q9JLQ4	Q9j1q4 mus musculu
14	44	49.4	133	11	Q91ZZ3	Q91zz3 mus musculu
15	44	49.4	182	5	Q9U558	Q9u558 plasmodium
16	44	49.4	336	10	Q8W4Z4	Q8w4z4 gossypium h
17	44	49.4	366	16	Q89Y61	Q89y61 bradyrhizob
18	44	49.4	418	5	Q8TA00	Q8ta00 trypanosoma
19	44	49.4	622	5	Q8TA01	Q8ta01 trypanosoma
20	44	49.4	671	10	Q9FXA2	Q9fxa2 arabidopsis
21	44	49.4	829	5	Q7YW24	Q7yw24 trypanosoma
22	44	49.4	833	5	Q8IFI2	Q8ifi2 trypanosoma
23	44	49.4	833	5	Q8IFI0	Q8ifi0 trypanosoma
24	44	49.4	834	5	Q8T9M8	Q8t9m8 trypanosoma
25	44	49.4	1058	12	Q805X6	Q805x6 simian herp
26	44	49.4	1058	12	Q7T5C7	Q7t5c7 simian herp
27	43	48.3	134	16	Q8Z588	Q8z588 salmonella
28	43	48.3	252	2	Q9S4T6	Q9s4t6 neisseria g
29	43	48.3	296	10	Q8W0W9	Q8w0w9 oryza sativ
30	43	48.3	331	5	Q8WRA5	Q8wra5 tetrahymena
31	43	48.3	470	2	Q84GW6	Q84gw6 lactobacill
32	43	48.3	470	4	Q8TDT2	Q8tdt2 homo sapien
33	43	48.3	471	2	Q84GU6	Q84gu6 lactobacill
34	43	48.3	472	2	Q84GW5	Q84gw5 lactobacill
35	43	48.3	472	10	Q94IQ3	Q94iq3 anemia phyl
36	43	48.3	473	2	Q84GV4	Q84gv4 lactobacill
37	43	48.3	473	2	Q84GV0	Q84gv0 lactobacill
38	43	48.3	473	2	Q84GU4	Q84gu4 lactobacill
39	43	48.3	474	2	Q84GV2	Q84gv2 lactobacill
40	43	48.3	475	2	Q84GV9	Q84gv9 lactobacill
41	43	48.3	475	2	Q84GV5	Q84gv5 lactobacill
42	43	48.3	476	2	Q84GU7	Q84gu7 lactobacill
43	43	48.3	477	2	Q84GW7	Q84gw7 lactobacill
44	43	48.3	478	2	Q84GW1	Q84gw1 lactobacill
45	43	48.3	478	2	Q84GV6	Q84gv6 lactobacill

ALIGNMENTS

RESULT 1

Q928G4

ID Q928G4 PRELIMINARY; PRT; 192 AA.
AC Q928G4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein lin2571.
 GN LIN2571.
 OS *Listeria innocua*.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; *Listeria*.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:849-852(2001).
 DR EMBL; AL596172; CAC97798.1; -.
 DR PIR; AF1753; AF1753.
 DR ListiList; LIN02571; -.
 DR InterPro; IPR006490; Tail_phil3.
 DR TIGRFAMS; TIGR01603; maj_tail_phil3; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 192 AA; 20841 MW; BEB4B4D3261DDA74 CRC64;

Query Match 53.4%; Score 47.5; DB 16; Length 192;
 Best Local Similarity 50.0%; Pred. No. 7.2;
 Matches 9; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

QY 3 TPQPL---LQVMMEPQGD 17
 ||:|| :::|||||
 Db 31 TPKPLPGGVEISVEPQGD 48

RESULT 2

Q84GV8

ID Q84GV8 PRELIMINARY; PRT; 473 AA.
 AC Q84GV8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS *Lactobacillus sakei* subsp. *carnosus*.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC *Lactobacillus*.
 OX NCBI_TaxID=214325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG489;
 RX MEDLINE=22458139; PubMed=12571056;
 RA Gevers D., Danielsen M., Huys G., Swings J.;

RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 RT from Different Types of Fermented Dry Sausage.";
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149583; AAN84487.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 473 473
 SQ SEQUENCE 473 AA; 53962 MW; 3F7AA0C3F577C133 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 473;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEP 14
 :: | |||: :||
 Db 246 IENPHPLLQITVEP 259

RESULT 3

Q84GV7

ID Q84GV7 PRELIMINARY; PRT; 473 AA.
 AC Q84GV7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS Lactobacillus sakei subsp. sakei.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=214326;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG493;
 RX MEDLINE=22458139; PubMed=12571056;
 RA Gevers D., Danielsen M., Huys G., Swings J.;
 RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 RT from Different Types of Fermented Dry Sausage.";
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149584; AAN84488.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 473 473

SQ SEQUENCE 473 AA; 53934 MW; EBA66C29002820EF CRC64;

Query Match 51.7%; Score 46; DB 2; Length 473;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | ||||: :||
Db 246 IENPHPLLQITVEP 259

RESULT 4

Q84GW2

ID Q84GW2 PRELIMINARY; PRT; 474 AA.
AC Q84GW2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tetracycline resistance protein (Fragment).
GN TETM.
OS Lactobacillus sakei subsp. carnosus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=214325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DG483;
RX MEDLINE=22458139; PubMed=12571056;
RA Gevers D., Danielsen M., Huys G., Swings J.;
RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
RT from Different Types of Fermented Dry Sausage."
RL Appl. Environ. Microbiol. 69:1270-1275(2003).
DR EMBL; AY149579; AAN84483.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
KW Cyclin.
FT NON_TER 1 1
FT NON_TER 474 474
SQ SEQUENCE 474 AA; 54076 MW; 4BCF7AA0C3F577C1 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 474;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | ||||: :||
Db 246 IENPHPLLQITVEP 259

RESULT 5

Q84GV1

ID Q84GV1 PRELIMINARY; PRT; 474 AA.

AC Q84GV1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG512;
 RX MEDLINE=22458139; PubMed=12571056;
 RA Gevers D., Danielsen M., Huys G., Swings J.;
 RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 from Different Types of Fermented Dry Sausage.";
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149590; AAN84494.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 474 474
 SQ SEQUENCE 474 AA; 54039 MW; E274A7732BD02820 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 474;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEP 14
 :: | |||: :||
 Db 246 IENPHPLLQITVEP 259

RESULT 6

Q84GW0

ID Q84GW0 PRELIMINARY; PRT; 475 AA.
 AC Q84GW0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS Lactobacillus sakei subsp. carnosus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=214325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG485;
 RX MEDLINE=22458139; PubMed=12571056;

RA Gevers D., Danielsen M., Huys G., Swings J.;
 RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 RT from Different Types of Fermented Dry Sausage.";
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149581; AAN84485.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 475 475
 SQ SEQUENCE 475 AA; 54190 MW; CDE3197026C272E0 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 475;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
 :: | |||: :||
 Db 248 IENPHPLLQITVEP 261

RESULT 7

Q84GU9

ID Q84GU9 PRELIMINARY; PRT; 475 AA.
 AC Q84GU9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS Lactobacillus sakei subsp. carnosus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=214325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG516;
 RX MEDLINE=22458139; PubMed=12571056;
 RA Gevers D., Danielsen M., Huys G., Swings J.;
 RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 RT from Different Types of Fermented Dry Sausage.";
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149592; AAN84496.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 DR GO; GO:0006414; P:translational elongation; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.

DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 475 475
 SQ SEQUENCE 475 AA; 54163 MW; AB4FF5EC84F7D570 CRC64;

 Query Match 51.7%; Score 46; DB 2; Length 475;
 Best Local Similarity 50.0%; Pred. No. 31;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 LQTPQPLLQVMMEP 14
 :: | |||: :||
 Db 251 IENPHPLLQITVEP 264

RESULT 8

Q84GW4

ID Q84GW4 PRELIMINARY; PRT; 477 AA.
 AC Q84GW4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS Lactobacillus sakei subsp. carnosus.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=214325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG143;
 RX MEDLINE=22458139; PubMed=12571056;
 RA Gevers D., Danielsen M., Huys G., Swings J.;
 RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 RT from Different Types of Fermented Dry Sausage."
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149577; AAN84481.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 DR GO; GO:0006414; P:translational elongation; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 477 477
 SQ SEQUENCE 477 AA; 54376 MW; 4DDED454C4D22EBB CRC64;

Query Match 51.7%; Score 46; DB 2; Length 477;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | ||||: :||
Db 249 IENPHPLLQITVEP 262

RESULT 9

Q84GW3

ID Q84GW3 PRELIMINARY; PRT; 477 AA.
AC Q84GW3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tetracycline resistance protein (Fragment).
GN TETM.
OS Lactobacillus sakei subsp. carnosus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=214325;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DG165;
RX MEDLINE=22458139; PubMed=12571056;
RA Gevers D., Danielsen M., Huys G., Swings J.;
RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
RT from Different Types of Fermented Dry Sausage.";
RL Appl. Environ. Microbiol. 69:1270-1275(2003).
DR EMBL; AY149578; AAN84482.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
KW Cyclin.
FT NON_TER 1 1
FT NON_TER 477 477
SQ SEQUENCE 477 AA; 54403 MW; E7AA08982E27715A CRC64;

Query Match 51.7%; Score 46; DB 2; Length 477;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | ||||: :||
Db 249 IENPHPLLQITVEP 262

RESULT 10

Q84GU5

ID Q84GU5 PRELIMINARY; PRT; 484 AA.
AC Q84GU5;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetracycline resistance protein (Fragment).
 GN TETM.
 OS Lactobacillus sakei subsp. sakei.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=214326;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DG525;
 RX MEDLINE=22458139; PubMed=12571056;
 RA Gevers D., Danielsen M., Huys G., Swings J.;
 RT "Molecular Characterization of tet(M) Genes in Lactobacillus Isolates
 RT from Different Types of Fermented Dry Sausage.";
 RL Appl. Environ. Microbiol. 69:1270-1275(2003).
 DR EMBL; AY149596; AAN84500.1; -.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 DR GO; GO:0006414; P:translational elongation; IEA.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 KW Cyclin.
 FT NON_TER 1 1
 FT NON_TER 484 484
 SQ SEQUENCE 484 AA; 55188 MW; 39E40238383A0F78 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 484;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEP 14
 :: | ||||: :||
 Db 251 IENPHPLLQITVEP 264

RESULT 11

O35745

ID O35745 PRELIMINARY; PRT; 667 AA.
 AC O35745;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Zinc finger protein regulator of apoptosis and cell cycle arrest.
 GN PLAGL1 OR ZAC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Pituitary;
 RX MEDLINE=97327559; PubMed=9184226;
 RA Spengler D., Villalba M., Hoffmann A., Pantaloni C., Houssami S.,
 RA Bockaert J., Journot L.;
 RT "Regulation of apoptosis and cell cycle arrest by Zacl, a novel zinc
 RT finger protein expressed in the pituitary gland and the brain."
 RL EMBO J. 16:2814-2825(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Pituitary;
 RA Spengler D., Villalba M., Hoffmann A., Pantaloni C., Houssami S.,
 RA Bockaert J., Journot L.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X95503; CAA64757.1; -.
 DR EMBL; X95504; CAA64758.1; -.
 DR MGD; MGI:1100874; Plagl1.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 7.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 667 AA; 75258 MW; 392F0AC979CBC10F CRC64;

Query Match 50.6%; Score 45; DB 11; Length 667;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LQTPQPLIQVMMEPQ 15
 | |||| | :||
 Db 543 LPVPQPLPQPQMPPQ 557

RESULT 12

Q9EPT3

ID Q9EPT3 PRELIMINARY; PRT; 675 AA.
 AC Q9EPT3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Lost on transformation protein 1.
 GN PLAGL1 OR ZAC1 OR LOT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH-Swiss;
 RX MEDLINE=20065118; PubMed=10597250;
 RA Abdollahi A., Bao R., Hamilton T.C.;
 RT "LOT1 is a growth suppressor gene down-regulated by the epidermal
 RT growth factor receptor ligands and encodes a nuclear zinc-finger
 RT protein."
 RL Oncogene 18:6477-6487(1999).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH-Swiss;
 RA Abdollahi A., Hamilton T.C.;
 RT "Identification of a splice variant of mouse Lot1 gene."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF324471; AAG48331.1; -.
 DR MGD; MGI:1100874; Plagl1.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 7.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; ZnF_C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 675 AA; 76109 MW; 0F467D165CA5B097 CRC64;

Query Match 50.6%; Score 45; DB 11; Length 675;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
 | |||| | |:
 Db 540 LPVPQPLPQPQMOPQ 554

RESULT 13

Q9JLQ4

ID Q9JLQ4 PRELIMINARY; PRT; 704 AA.
 AC Q9JLQ4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Zinc finger protein ZAC1.
 GN PLAGL1 OR ZAC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20136063; PubMed=10669760;
 RA Huang S.-M., Stallcup M.R.;
 RT "Mouse Zacl, a Transcriptional Coactivator and Repressor for Nuclear
 RT Receptors."
 RL Mol. Cell. Biol. 20:1855-1867(2000).
 DR EMBL; AF147785; AAF34245.1; -.
 DR TRANSFAC; T05150; -.
 DR MGD; MGI:1100874; Plagl1.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 7.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; ZnF_C2H2; 7.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 704 AA; 79214 MW; 3AF88262D504FA80 CRC64;

Query Match 50.6%; Score 45; DB 11; Length 704;
Best Local Similarity 60.0%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
| | | | | | : | |
Db 543 LPVPQPLPQPQMOPQ 557

RESULT 14

Q91ZZ3

ID Q91ZZ3 PRELIMINARY; PRT; 133 AA.
AC Q91ZZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-synuclein (Synuclein, beta).
GN A1838531 OR SNCB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21367613; PubMed=11474193;
RA Sopher B.L., Koszdin K.L., McClain M.E., Myrick S.B., Martinez R.A.,
RA Smith A.C., La Spada A.R.;
RT "Genomic organization, chromosome location, and expression analysis of
RT mouse beta-synuclein, a candidate for involvement in
RT neurodegeneration.";
RL Cytogenet. Cell Genet. 93:117-123(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF348164; AAK83238.1; -.
DR EMBL; AF348162; AAK83238.1; JOINED.
DR EMBL; AF348163; AAK83238.1; JOINED.
DR EMBL; BC019409; AAH19409.1; -.
DR MGD; MGI:1889011; Sncb.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR InterPro; IPR001058; Synuclein.
DR Pfam; PF01387; Synuclein; 1.
DR PRINTS; PR01211; SYNUCLEIN.
DR ProDom; PD010631; Synuclein; 1.
SQ SEQUENCE 133 AA; 14052 MW; 8274D8A6A0D8E4D5 CRC64;

Query Match 49.4%; Score 44; DB 11; Length 133;
Best Local Similarity 46.2%; Pred. No. 19;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
: | | : : | | : | :
Db 104 EPLIEPLMEPEGE 116

RESULT 15

Q9U558

ID Q9U558 PRELIMINARY; PRT; 182 AA.
 AC Q9U558;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Merozoite surface protein 1 (Fragment).
 GN MSP-1.
 OS Plasmodium vivax.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5855;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KPV97-73;
 RA Kim S.H., Kwon S.I.;
 RT "Analysis of the Plasmodium vivax merozoite surface protein 1 gene
 RT sequence from resurgent Korean isolates."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KPV97-73;
 RA Lee K.N., Song K.J., Song J.W., Lim C.S.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF098282; AAF25530.1; -.
 FT NON_TER 1 1
 FT NON_TER 182 182
 SQ SEQUENCE 182 AA; 19514 MW; 2BB8A7A12D4471C5 CRC64;

Query Match 49.4%; Score 44; DB 5; Length 182;
 Best Local Similarity 56.2%; Pred. No. 26;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QTPQPLLQVMMEPQGD 17
 | ||| ||: | ||
 Db 56 QQPQPQSQVVPAPAGD 71

Search completed: August 24, 2004, 15:50:26
 Job time : 54.5224 secs

OM protein - protein search, using sw model

Run on: August 24, 2004, 14:57:04 ; Search time 9.13433 Seconds
 (without alignments)
 96.908 Million cell updates/sec

Title: US-09-641-801-2
 Perfect score: 89
 Sequence: 1 LQTPQPLLQVMMEPQGD 17

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	48	53.9	691	1	EFG_STRPY	P82477 streptococc
2	48	53.9	692	1	EFG_STRA3	Q8e3e7 streptococc
3	48	53.9	692	1	EFG_STRA5	Q8dxs7 streptococc
4	48	53.9	693	1	EFG_STRMU	Q8dvv4 streptococc
5	48	53.9	709	1	EFG_LACLA	Q9cdg1 lactococcus
6	46	51.7	639	1	TETM_UREUR	P09757 ureaplasma
7	46	51.7	693	1	EFG_STRPN	Q97sq3 streptococc
8	44	49.4	134	1	SYUB_BOVIN	P33567 bos taurus
9	44	49.4	134	1	SYUB_HUMAN	Q16143 homo sapien
10	44	49.4	137	1	SYUB_RAT	Q63754 rattus norv
11	43	48.3	437	1	CAH9_MOUSE	Q8vhh5 mus musculu
12	43	48.3	639	1	TET9_ENTFA	P21598 enterococcu
13	43	48.3	639	1	TETM_STAAM	Q932i8 staphylococ
14	43	48.3	639	1	TETM_STAAU	Q53770 staphylococ
15	43	48.3	695	1	EFG_LISIN	Q927i5 listeria in
16	43	48.3	695	1	EFG_LISMO	Q8y421 listeria mo
17	43	48.3	699	1	EFG_AGRT5	Q8ue15 agrobacteri

18	43	48.3	699	1	EFG_AGRTU	P70782	agrobacteri
19	43	48.3	699	1	EFG_RHIME	Q92qh2	rhizobium m
20	42	47.2	643	1	VP40_HSVE2	P52369	equine herp
21	42	47.2	698	1	EFG_VIBCH	Q9kuz7	vibrio chol
22	42	47.2	699	1	EFG_VIBPA	Q87l45	vibrio para
23	42	47.2	699	1	EFG_VIBVU	Q8dcq8	vibrio vuln
24	41	46.1	78	1	YHGG_ECOLI	P46845	escherichia
25	41	46.1	544	1	TCPG_DROME	P48605	drosophila
26	41	46.1	639	1	TET5_ENTFA	P11131	enterococcu
27	41	46.1	639	1	TETM_STRPN	Q54807	streptococc
28	41	46.1	641	1	TETS_LISMO	Q48791	listeria mo
29	41	46.1	646	1	TETS_LACLA	Q48712	lactococcus
30	41	46.1	693	1	EFG_ENTFA	Q839g9	enterococcu
31	41	46.1	698	1	EFG_LACPL	Q88xy8	lactobacill
32	41	46.1	857	1	CAPP_THES7	P51060	thermus sp.
33	41	46.1	1058	1	UL52_HSV11	P10236	herpes simp
34	41	46.1	1653	1	YFHM_ECOLI	P76578	escherichia
35	40.5	45.5	656	1	PTPR_MOUSE	Q62132	mus musculu
36	40.5	45.5	656	1	PTPR_RAT	O08617	rattus norv
37	40.5	45.5	657	1	PTPR_HUMAN	Q15256	homo sapien
38	40	44.9	282	1	LGUL_BRAOL	Q39366	brassica ol
39	40	44.9	357	1	YAUH_SCHPO	Q10170	schizosacch
40	40	44.9	422	1	RBN_XANAC	Q8pnv2	xanthomonas
41	40	44.9	425	1	RBN_XANCP	Q8pc75	xanthomonas
42	40	44.9	671	1	Z282_HUMAN	Q9udv7	homo sapien
43	40	44.9	691	1	EFG2_SYNY3	P74228	synechocyst
44	40	44.9	691	1	EFG_THETH	P13551	thermus the
45	40	44.9	696	1	EFG_RHILO	Q98n59	rhizobium l

ALIGNMENTS

RESULT 1

EFG_STRPY

ID EFG_STRPY STANDARD; PRT; 691 AA.
AC P82477;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Elongation factor G (EF-G).
GN FUS OR FUSA OR SPY0273 OR SPYM3_0200 OR SPS0206 OR SPYM18_0260.
OS Streptococcus pyogenes,
OS Streptococcus pyogenes (serotype M3), and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 198466, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206;
 RA Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SSI-1 / Serotype M3;
 RX MEDLINE=22683278; PubMed=12799345;
 RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayashi H., Hattori M., Hamada S.;
 RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 RT large-scale genomic rearrangement in invasive strains and new insights
 RT into phage evolution.";
 RL Genome Res. 13:1042-1055(2003).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108;
 RA Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 RN [5]
 RP PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
 RC STRAIN=JRS4 / Serotype M6;
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
 RA VanBogelen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
 RT proteins.";
 RL Submitted (MAY-2000) to Swiss-Prot.
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
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DR EMBL; AE006493; AAK33347.1; -.
DR EMBL; AE014140; AAM78807.1; -.
DR EMBL; AP005141; BAC63301.1; -.
DR EMBL; AE009973; AAL97040.1; -.
DR HSSP; P13551; 1DAR.
DR HAMAP; MF_00054; -; 1.
DR InterPro; IPR004540; EF-G.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR TIGRFAMs; TIGR00484; EF-G; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFACTOR_GTP; 1.
KW Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT INIT_MET 0 0
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 80 84 GTP (BY SIMILARITY).
FT NP_BIND 134 137 GTP (BY SIMILARITY).
SQ SEQUENCE 691 AA; 76397 MW; D59B857A2CDB40CD CRC64;

Query Match 53.9%; Score 48; DB 1; Length 691;

Best Local Similarity 40.0%; Pred. No. 2.9;

Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQ 15

:: |:|::|:|:|:

Db 399 IEVPEPVIQLMVEPK 413

RESULT 2

EFG_STR3

ID EFG_STR3 STANDARD; PRT; 692 AA.
AC Q8E3E7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Elongation factor G (EF-G).
GN FUSA OR GBS1812.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;

```

RX  MEDLINE=22242508; PubMed=12354221;
RA  Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA  Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA  Kunst F.;
RT  "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT  invasive neonatal disease.";
RL  Mol. Microbiol. 45:1499-1513(2002).
CC  -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC      the nascent protein chain from the A-site to the P-site of the
CC      ribosome.
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC      EF-G/EF-2 subfamily.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AL766853; CAD47471.1; -.
DR  SagaList; gbs1812; -.
DR  HAMAP; MF_00054; -; 1.
DR  InterPro; IPR004540; EF-G.
DR  InterPro; IPR000795; EF_GTPbind.
DR  InterPro; IPR000640; EFG_C.
DR  InterPro; IPR009022; EFG_III_V.
DR  InterPro; IPR005517; EFG_IV.
DR  InterPro; IPR004161; EFTU_D2.
DR  InterPro; IPR005225; Small_GTP.
DR  InterPro; IPR009000; Translat_factor.
DR  Pfam; PF00679; EFG_C; 1.
DR  Pfam; PF03764; EFG_IV; 1.
DR  Pfam; PF00009; GTP_EFTU; 1.
DR  Pfam; PF03144; GTP_EFTU_D2; 1.
DR  PRINTS; PR00315; ELONGATNFCT.
DR  TIGRFAMs; TIGR00484; EF-G; 1.
DR  TIGRFAMs; TIGR00231; small_GTP; 1.
DR  PROSITE; PS00301; EFACITOR_GTP; 1.
KW  Elongation factor; Protein biosynthesis; GTP-binding;
KW  Complete proteome.
FT  NP_BIND      17      24      GTP (BY SIMILARITY).
FT  NP_BIND      81      85      GTP (BY SIMILARITY).
FT  NP_BIND     135     138      GTP (BY SIMILARITY).
SQ  SEQUENCE     692 AA;  76598 MW;  199DA941BC7F9182 CRC64;

```

```

Query Match          53.9%;  Score 48;  DB 1;  Length 692;
Best Local Similarity 40.0%;  Pred. No. 2.9;
Matches      6;  Conservative      8;  Mismatches      1;  Indels      0;  Gaps      0;

```

```

Qy      1 LQTPQPLLQVMMEPQ 15
        :: |:|::|:|:|:|:
Db      400 IEVPEPVIQLMVEPK 414

```


RESULT 3

EFG_STRA5

ID EFG_STRA5 STANDARD; PRT; 692 AA.

AC Q8DXS7;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Elongation factor G (EF-G).

GN FUSA OR SAG1769.

OS *Streptococcus agalactiae* (serotype V).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC *Streptococcus*.

OX NCBI_TaxID=216466;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2603 V/R / Serotype V;

RX MEDLINE=22222988; PubMed=12200547;

RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,

RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,

RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,

RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,

RA Fraser C.M.;

RT "Complete genome sequence and comparative genomic analysis of an

RT emerging human pathogen, serotype V *Streptococcus agalactiae*.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).

CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of

CC the nascent protein chain from the A-site to the P-site of the

CC ribosome.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.

CC EF-G/EF-2 subfamily.

CC -----
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 CC -----

DR EMBL; AE014272; AAN00632.1; -.

DR TIGR; SAG1769; -.

DR HAMAP; MF_00054; -; 1.

DR InterPro; IPR004540; EF-G.

DR InterPro; IPR000795; EF_GTPbind.

DR InterPro; IPR000640; EFG_C.

DR InterPro; IPR009022; EFG_III_V.

DR InterPro; IPR005517; EFG_IV.

DR InterPro; IPR004161; EFTU_D2.

DR InterPro; IPR005225; Small_GTP.

DR InterPro; IPR009000; Translat_factor.

DR Pfam; PF00679; EFG_C; 1.

DR Pfam; PF03764; EFG_IV; 1.

DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFAMs; TIGR00484; EF-G; 1.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFACTOR_GTP; 1.
 KW Elongation factor; Protein biosynthesis; GTP-binding;
 KW Complete proteome.
 FT NP_BIND 17 24 GTP (BY SIMILARITY).
 FT NP_BIND 81 85 GTP (BY SIMILARITY).
 FT NP_BIND 135 138 GTP (BY SIMILARITY).
 SQ SEQUENCE 692 AA; 76570 MW; 36BCF199BA006AB1 CRC64;

Query Match 53.9%; Score 48; DB 1; Length 692;
 Best Local Similarity 40.0%; Pred. No. 2.9;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEPQ 15
 :: |:|::|:|:|:
 Db 400 IEVPEPVIQIMVEPK 414

RESULT 4

EFG_STRMU

ID EFG_STRMU STANDARD; PRT; 693 AA.
 AC Q8DVV4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Elongation factor G (EF-G).
 GN FUSA OR SMU.359.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;
 RX MEDLINE=22295063; PubMed=12397186;
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
 RT pathogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
 CC -----
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CC -----

DR EMBL; AE014883; AAN58117.1; -.
DR HAMAP; MF_00054; -; 1.
DR InterPro; IPR004540; EF-G.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR TIGRFAMs; TIGR00484; EF-G; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFACTOR_GTP; 1.
KW Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
FT NP_BIND 135 138 GTP (BY SIMILARITY).
SQ SEQUENCE 693 AA; 76664 MW; 252763A2606E5E04 CRC64;

Query Match 53.9%; Score 48; DB 1; Length 693;
Best Local Similarity 40.0%; Pred. No. 2.9;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQ 15
:: |:|::|:|:|:
Db 400 IEVPEPVIQLMVEPK 414

RESULT 5

EFG_LACLA

ID EFG_LACLA STANDARD; PRT; 709 AA.
AC Q9CDG1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G).
GN FUSA OR LL2260.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";

RL Genome Res. 11:731-753(2001).
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
 CC -----
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 CC -----
 DR EMBL; AE006455; AAK06358.1; -.
 DR PIR; D86907; D86907.
 DR HSSP; P13551; 1DAR.
 DR HAMAP; MF_00054; -; 1.
 DR InterPro; IPR004540; EF-G.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR000640; EFG_C.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR005225; Small_GTP.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF00679; EFG_C; 1.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFAMs; TIGR00484; EF-G; 1.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFACTOR_GTP; 1.
 KW Elongation factor; Protein biosynthesis; GTP-binding;
 KW Complete proteome.
 FT NP_BIND 17 24 GTP (BY SIMILARITY).
 FT NP_BIND 81 85 GTP (BY SIMILARITY).
 FT NP_BIND 135 138 GTP (BY SIMILARITY).
 SQ SEQUENCE 709 AA; 77955 MW; 1EAD29D65A748032 CRC64;

Query Match 53.9%; Score 48; DB 1; Length 709;
 Best Local Similarity 40.0%; Pred. No. 3;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQ 15
 :: |:|::|:|:|:
 Db 415 IEVPEPVIQLMVEPK 429

RESULT 6

TETM_UREUR

ID TETM_UREUR STANDARD; PRT; 639 AA.

AC P09757;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tetracycline resistance protein tetM.
 GN TETM.
 OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=2130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88144009; PubMed=3344217;
 RA Sanchez-Pescador R., Brown J.T., Roberts M., Urdea M.S.;
 RT "The nucleotide sequence of the tetracycline resistance determinant
 RT tetM from Ureaplasma urealyticum.";
 RL Nucleic Acids Res. 16:1216-1217(1988).
 CC -!- FUNCTION: Abolishes the inhibitory effect of tetracyclin on
 CC protein synthesis by a non-covalent modification of the ribosomes.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC TetM/tetO subfamily.
 CC -----
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 CC -----
 DR EMBL; U08812; AAA73978.1; -.
 DR PIR; S03268; S03268.
 DR HSSP; P13551; 1FNM.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR000640; EFG_C.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR005225; Small_GTP.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF00679; EFG_C; 1.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFACTOR_GTP; 1.
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 74 78 GTP (BY SIMILARITY).
 FT NP_BIND 128 131 GTP (BY SIMILARITY).
 SQ SEQUENCE 639 AA; 72599 MW; A1497055BB182B3A CRC64;

Query Match 51.7%; Score 46; DB 1; Length 639;
 Best Local Similarity 50.0%; Pred. No. 5.7;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
 :: | ||||: |||
 Db 339 IENPHPLLQITVEP 352

RESULT 7

EFG_STRPN

ID EFG_STRPN STANDARD; PRT; 693 AA.
AC Q97SQ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G).
GN FUSA OR SP0273 OR SPRO250.
OS Streptococcus pneumoniae, and
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313, 171101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczyk L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC the nascent protein chain from the A-site to the P-site of the
CC ribosome.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EF-G/EF-2 subfamily.

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CC -----

DR EMBL; AE007340; AAK74451.1; -.
DR EMBL; AE008406; AAK99054.1; -.
DR PIR; B95032; B95032.
DR PIR; B97903; B97903.
DR TIGR; SP0273; -.
DR HAMAP; MF_00054; -; 1.
DR InterPro; IPR004540; EF-G.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR TIGRFAMs; TIGR00484; EF-G; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR PROSITE; PS00301; EFACITOR_GTP; 1.
KW Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
FT NP_BIND 135 138 GTP (BY SIMILARITY).
SQ SEQUENCE 693 AA; 76831 MW; 73187D0287AC6193 CRC64;

Query Match 51.7%; Score 46; DB 1; Length 693;
Best Local Similarity 40.0%; Pred. No. 6.2;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPQPLLQVMMEPQ 15
: |:|::|:|:|:
Db 400 INVPEPVIQIMVEPK 414

RESULT 8

SYUB_BOVIN

ID SYUB_BOVIN STANDARD; PRT; 134 AA.
AC P33567;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-synuclein (Phosphoneuroprotein 14) (PNP 14) (14 kDa brain-
DE specific protein).
GN SNCB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94039126; PubMed=8223629;
 RA Nakajo S., Tsukada K., Omata K., Nakamura Y., Nakaya K.;
 RT "A new brain-specific 14-kDa protein is a phosphoprotein. Its
 RT complete amino acid sequence and evidence for phosphorylation."
 RL Eur. J. Biochem. 217:1057-1063(1993).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=91038084; PubMed=2230807;
 RA Nakajo S., Omata K., Aiuchi T., Shibayama T., Okahashi I., Ochiai H.,
 RA Nakai Y., Nakaya K., Nakamura Y.;
 RT "Purification and characterization of a novel brain-specific 14-kDa
 RT protein."
 RL J. Neurochem. 55:2031-2038(1990).
 CC -!- FUNCTION: May be involved in neuronal plasticity.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Specifically present in synapses around
 CC neurons but not in glial cells.
 CC -!- PTM: Phosphorylated. Phosphorylation by G-protein coupled receptor
 CC kinases (GRK) is more efficient than phosphorylation by CK1, CK2
 CC and CaM-kinase II (By similarity).
 CC -!- SIMILARITY: Belongs to the synuclein family.
 DR PIR; A60218; A60218.
 DR PIR; S39046; S39046.
 DR InterPro; IPR001058; Synuclein.
 DR Pfam; PF01387; Synuclein; 1.
 DR PRINTS; PR01211; SYNUCLEIN.
 DR ProDom; PD010631; Synuclein; 1.
 KW Phosphorylation; Repeat.
 FT DOMAIN 20 67 4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-K-
 FT [EQ]-[GQ]-V-X(4).
 FT REPEAT 20 30 1.
 FT REPEAT 31 41 2.
 FT REPEAT 42 56 3 (APPROXIMATE).
 FT REPEAT 57 67 4.
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CK2, BARK1 AND GRK5)
 FT (BY SIMILARITY).
 SQ SEQUENCE 134 AA; 14277 MW; 484FA01A01979966 CRC64;

Query Match 49.4%; Score 44; DB 1; Length 134;
 Best Local Similarity 46.2%; Pred. No. 2.4;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 QPLLQVMMEPQGD 17
 :||:::||||:
 Db 105 EPLIEPLMEPEGE 117

RESULT 9

SYUB_HUMAN

ID SYUB_HUMAN STANDARD; PRT; 134 AA.
 AC Q16143;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Beta-synuclein.
 GN SNCB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94252398; PubMed=8194594;
 RA Jakes R., Spillantini M.G., Goedert M.;
 RT "Identification of two distinct synucleins from human brain.";
 RL FEBS Lett. 345:27-32(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99026142; PubMed=9806846;
 RA Lavedan C., Leroy E., Torres R., Dehejia A., Dutra A., Buchholtz S.,
 RA Nussbaum R.L., Polymeropoulos M.H.;
 RT "Genomic organization and expression of the human beta-synuclein gene
 RT (SNCB).";
 RL Genomics 54:173-175(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
 RT vector.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP PHOSPHORYLATION.
 RX MEDLINE=20409007; PubMed=10852916;

RA Pronin A.N., Morris A.J., Surguchov A., Benovic J.L.;
 RT "Synucleins are a novel class of substrates for G protein-coupled
 RT receptor kinases.";
 RL J. Biol. Chem. 275:26515-26522(2000).
 CC -!- FUNCTION: Non amyloid component of senile plaques found in
 CC Alzheimer's disease. Could act as a regulator of SNCA aggregation
 CC process. Protects neurons from staurosporine and 6 hydroxy
 CC dopamine (6OHDA)-stimulated caspase activation in a p53-dependent
 CC manner. Contributes to restore the SNCA anti-apoptotic function
 CC abolished by 6OHDA. Not found in the Lewy bodies associated with
 CC Parkinson's disease.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in brain; concentrated
 CC in presynaptic nerve terminals.
 CC -!- PTM: Phosphorylated. Phosphorylation by G-protein coupled receptor
 CC kinases (GRK) is more efficient than phosphorylation by CK1, CK2
 CC and CaM-kinase II.
 CC -!- DISEASE: Brain iron accumulation type 1 (NBIA1, also called
 CC Hallervorden-Spatz syndrome), a rare neuroaxonal dystrophy, is
 CC histologically characterized by axonal spheroids, iron deposition,
 CC Lewy body (LB)-like intraneuronal inclusions, glial inclusions and
 CC neurofibrillary tangles. SNCB is found in spheroids but not in
 CC inclusions.
 CC -!- SIMILARITY: Belongs to the synuclein family.
 CC -----
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 CC -----
 DR EMBL; S69965; AAB30860.1; -.
 DR EMBL; AF053136; AAC80286.1; -.
 DR EMBL; AF053134; AAC80286.1; JOINED.
 DR EMBL; AF053135; AAC80286.1; JOINED.
 DR EMBL; BT006627; AAP35273.1; -.
 DR EMBL; BC002902; AAH02902.1; -.
 DR PIR; S44430; S44430.
 DR Genew; HGNC:11140; SNCB.
 DR MIM; 602569; -.
 DR GO; GO:0004859; F:phospholipase inhibitor activity; TAS.
 DR InterPro; IPR001058; Synuclein.
 DR Pfam; PF01387; Synuclein; 1.
 DR PRINTS; PR01211; SYNUCLEIN.
 DR ProDom; PD010631; Synuclein; 1.
 KW Phosphorylation; Repeat.
 FT DOMAIN 20 67 4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-K-
 FT [EQ]-[GQ]-V-X(4).
 FT REPEAT 20 30 1.
 FT REPEAT 31 41 2.
 FT REPEAT 42 56 3 (APPROXIMATE).
 FT REPEAT 57 67 4.
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CK2, BARK1 AND GRK5).
 SQ SEQUENCE 134 AA; 14288 MW; 5BCA9FCA615AC4EF CRC64;

Query Match 49.4%; Score 44; DB 1; Length 134;
Best Local Similarity 46.2%; Pred. No. 2.4;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
:|:::|::|:
Db 105 EPLIEPLMEPEGE 117

RESULT 10

SYUB_RAT

ID SYUB_RAT STANDARD; PRT; 137 AA.
AC Q63754;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-synuclein (Phosphoneuroprotein 14) (PNP 14).
GN SNCB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93019240; PubMed=1402909;
RA Tobe T., Nakajo S., Tanaka A., Mitoya A., Omata K., Nakaya K.,
RA Tomita M., Nakamura Y.;
RT "Cloning and characterization of the cDNA encoding a novel brain-
RT specific 14-kDa protein.";
RL J. Neurochem. 59:1624-1629(1992).
RN [2]
RP PHOSPHORYLATION BY CAM-KINASE II.
RX MEDLINE=94039126; PubMed=8223629;
RA Nakajo S., Tsukada K., Omata K., Nakamura Y., Nakaya K.;
RT "A new brain-specific 14-kDa protein is a phosphoprotein. Its complete
RT amino acid sequence and evidence for phosphorylation.";
RL Eur. J. Biochem. 217:1057-1063(1993).
CC -!- FUNCTION: May be involved in neuronal plasticity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed specifically in brain.
CC -!- PTM: Phosphorylated. Phosphorylation by G-protein coupled receptor
CC kinases (GRK) is more efficient than phosphorylation by CK1, CK2
CC and CaM-kinase II.
CC -!- SIMILARITY: Belongs to the synuclein family.
CC -----
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CC -----
DR EMBL; D17764; BAA04610.1; -.
DR InterPro; IPR001058; Synuclein.
DR Pfam; PF01387; Synuclein; 1.

DR PRINTS; PR01211; SYNUCLEIN.
 DR ProDom; PD010631; Synuclein; 1.
 KW Phosphorylation; Repeat.
 FT DOMAIN 20 67 4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-K-
 FT [EQ]-[GQ]-V-X(4).
 FT REPEAT 20 30 1.
 FT REPEAT 31 41 2.
 FT REPEAT 42 56 3 (APPROXIMATE).
 FT REPEAT 57 67 4.
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CK2, BARK1 AND GRK5)
 FT (BY SIMILARITY).
 SQ SEQUENCE 137 AA; 14504 MW; 678C6CB84FA01A03 CRC64;

Query Match 49.4%; Score 44; DB 1; Length 137;
 Best Local Similarity 46.2%; Pred. No. 2.5;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 5 QPLLQVMMEPQGD 17
 :||:::||||:
 Db 105 EPLIEPLMEPEGE 117

RESULT 11

CAH9_MOUSE

ID CAH9_MOUSE STANDARD; PRT; 437 AA.
 AC Q8VHB5; Q8K1G1; Q8VDE4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Carbonic anhydrase IX precursor (EC 4.2.1.1) (Carbonate dehydratase
 DE IX) (CA-IX) (CAIX) (Membrane antigen MN homolog).
 GN CA9 OR CAR9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=129/Ola;
 RX PubMed=14604546;
 RA Zat'ovicova M., Tarabkova K., Svastova E., Gibadulinova A., Mucha V.,
 RA Jakubickova L., Biesova Z., Rafajova M., Ortova Gut M.O., Parkkila S.,
 RA Parkkila A.-K., Waheed A., Sly W.S., Horak I., Pastorek J.,
 RA Pastorekova S.;
 RT "Monoclonal antibodies generated in carbonic anhydrase IX-deficient
 RT mice recognize different domains of tumour-associated hypoxia-induced
 RT carbonic anhydrase IX."
 RL J. Immunol. Methods 282:117-134(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Ortova M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=ICR; TISSUE=Small intestine;
 RA Wang Y.P., Yoshikawa K., Kozaki K., Miyaishi O., Nakagawa A.,
 RA Muramatsu H., Kawada Y., Uchida K., Nishikawa N., Saga S.;

RT "Alternative spliced mRNA coding for MN/CA9."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Reversible hydration of carbon dioxide (By similarity).
 CC -!- CATALYTIC ACTIVITY: H(2)CO(3) = CO(2) + H(2)O.
 CC -!- COFACTOR: Zinc (By similarity).
 CC -!- SUBUNIT: Forms oligomers linked by disulfide bonds (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8VHB5-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8VHB5-2; Sequence=VSP_007409, VSP_007410;
 CC -!- SIMILARITY: Belongs to the eukaryotic-type carbonic anhydrase
 CC family.

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 CC -----

DR EMBL; AY049077; AAL14193.1; -.
 DR EMBL; AJ245857; CAC80975.1; -.
 DR EMBL; AB086322; BAC00816.1; -.
 DR MGD; MGI:2447188; Car9.
 DR InterPro; IPR001148; Euk_COanhd.
 DR Pfam; PF00194; carb_anhydrase; 1.
 DR ProDom; PD000865; Euk_COanhd; 1.
 DR PROSITE; PS00162; EUK_CO2_ANHYDRASE; 1.
 KW Lyase; Zinc; Transmembrane; Glycoprotein; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 437 CARBONIC ANHYDRASE IX.
 FT METAL 205 205 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 207 207 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 230 230 ZINC (CATALYTIC) (BY SIMILARITY).
 FT TRANSMEM 391 411 POTENTIAL.
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 282 282 G -> V (in isoform 2).
 FT /FTId=VSP_007409.
 FT VARSPLIC 283 437 Missing (in isoform 2).
 FT /FTId=VSP_007410.
 SQ SEQUENCE 437 AA; 47264 MW; 88F23380DCD35344 CRC64;

Query Match 48.3%; Score 43; DB 1; Length 437;
 Best Local Similarity 45.8%; Pred. No. 12;
 Matches 11; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 1 LQTPQP-----LLQVMMEPQG 16
 | || | |||| :|||
 Db 12 LSTPAPTALLLLFLLLQVSAQPQG 35

RESULT 12

TET9_ENTFA

ID TET9_ENTFA STANDARD; PRT; 639 AA.

AC P21598;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tetracycline resistance protein tetM from transposon Tn916

DE (TetM(916)).

GN TETM OR TET(M).

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI_TaxID=1351;

RN [1]

RP SEQUENCE FROM N.A.

RC TRANSPOSON=Tn916;

RX MEDLINE=91045089; PubMed=2172929;

RA Burdett V.;

RT "Nucleotide sequence of the tet(M) gene of Tn916.";

RL Nucleic Acids Res. 18:6137-6137(1990).

CC -!- FUNCTION: Abolishes the inhibitory effect of tetracyclin on

CC protein synthesis by a non-covalent modification of the ribosomes.

CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.

CC TetM/tetO subfamily.

CC -----

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CC -----

DR EMBL; X56353; CAA39796.1; -.

DR PIR; S13142; S13142.

DR HSSP; P13551; 1FNM.

DR InterPro; IPR000795; EF_GTPbind.

DR InterPro; IPR000640; EFG_C.

DR InterPro; IPR009022; EFG_III_V.

DR InterPro; IPR005517; EFG_IV.

DR InterPro; IPR004161; EFTU_D2.

DR InterPro; IPR005225; Small_GTP.

DR InterPro; IPR009000; Translat_factor.

DR Pfam; PF00679; EFG_C; 1.

DR Pfam; PF03764; EFG_IV; 1.

DR Pfam; PF00009; GTP_EFTU; 1.

DR Pfam; PF03144; GTP_EFTU_D2; 1.

DR PRINTS; PR00315; ELONGATNFCT.

DR TIGRFAMs; TIGR00231; small_GTP; 1.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

KW Protein biosynthesis; Antibiotic resistance; GTP-binding;

KW Transposable element.

FT NP_BIND 10 17 GTP (BY SIMILARITY).

FT NP_BIND 74 78 GTP (BY SIMILARITY).

FT NP_BIND 128 131 GTP (BY SIMILARITY).

SQ SEQUENCE 639 AA; 72464 MW; B2315A37B53B18FB CRC64;

Query Match 48.3%; Score 43; DB 1; Length 639;

Best Local Similarity 50.0%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
:: | ||| :||
Db 339 IENPHPLLQTTVEP 352

RESULT 13

TETM_STAAM

ID TETM_STAAM STANDARD; PRT; 639 AA.
AC Q932I8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tetracycline resistance protein tetM (TetA(M)).
GN TETM OR SAV0398.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of meticillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- FUNCTION: Abolishes the inhibitory effect of tetracyclin on
CC protein synthesis by a non-covalent modification of the ribosomes
CC (By similarity).
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC TetM/tetO subfamily.
CC -----
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CC -----
DR EMBL; AP003359; BAB56560.1; -.
DR InterPro; IPR000640; EFG_C.
DR InterPro; IPR009022; EFG_III_V.
DR InterPro; IPR005517; EFG_IV.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR000795; EF_GTPbind.
DR InterPro; IPR005225; Small_GTP.
DR InterPro; IPR009000; Translat_factor.
DR Pfam; PF00679; EFG_C; 1.
DR Pfam; PF03764; EFG_IV; 1.

DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFATOR GTP; 1.
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding;
 KW Complete proteome.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 74 78 GTP (BY SIMILARITY).
 FT NP_BIND 128 131 GTP (BY SIMILARITY).
 SQ SEQUENCE 639 AA; 72549 MW; 1A97DD13A673BE1F CRC64;

Query Match 48.3%; Score 43; DB 1; Length 639;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
 :: | |||| :||
 Db 339 IENPHPLLQTTVEP 352

RESULT 14

TETM_STAAU

ID TETM_STAAU STANDARD; PRT; 639 AA.
 AC Q53770;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tetracycline resistance protein tetM (TetA(M)).
 GN TETM OR TETA(M).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91158314; PubMed=2073121;
 RA Nesin M., Svec P., Lupski J.R., Godson G.N., Kreiswirth B.,
 RA Projan S.J.;
 RT "Cloning and nucleotide sequence of a chromosomally encoded
 RT tetracycline resistance determinant, tetA(M), from a pathogenic,
 RT methicillin-resistant strain of Staphylococcus aureus."
 RL Antimicrob. Agents Chemother. 34:2273-2276(1990).
 CC -!- FUNCTION: Abolishes the inhibitory effect of tetracyclin on
 CC protein synthesis by a non-covalent modification of the ribosomes.
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC TetM/tetO subfamily.
 CC -----
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 CC -----
 DR EMBL; M21136; AAA26678.1; -.
 DR PIR; A60633; A60633.

DR HSSP; P13551; 1FNM.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR000640; EFG_C.
 DR InterPro; IPR009022; EFG_III_V.
 DR InterPro; IPR005517; EFG_IV.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR005225; Small_GTP.
 DR InterPro; IPR009000; Translat_factor.
 DR Pfam; PF00679; EFG_C; 1.
 DR Pfam; PF03764; EFG_IV; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFACTOR_GTP; 1.
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 74 78 GTP (BY SIMILARITY).
 FT NP_BIND 128 131 GTP (BY SIMILARITY).
 SQ SEQUENCE 639 AA; 72639 MW; 66470062A673BE1F CRC64;

Query Match 48.3%; Score 43; DB 1; Length 639;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPQPLLQVMMEP 14
 :: | |||| :||
 Db 339 IENPHPLLQTTVEP 352

RESULT 15

EFG_LISIN

ID EFG_LISIN STANDARD; PRT; 695 AA.
 AC Q927I5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G).
 GN FUSA OR FUS OR LIN2803.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

```

RT  "Comparative genomics of Listeria species.";
RL  Science 294:849-852(2001).
CC  -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC      the nascent protein chain from the A-site to the P-site of the
CC      ribosome.
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC      EF-G/EF-2 subfamily.
CC  -----
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CC  -----
DR  EMBL; AL596173; CAC98029.1; -.
DR  PIR; AE1782; AE1782.
DR  ListiList; LIN02803; -.
DR  HAMAP; MF_00054; -; 1.
DR  InterPro; IPR004540; EF-G.
DR  InterPro; IPR000795; EF_GTPbind.
DR  InterPro; IPR000640; EFG_C.
DR  InterPro; IPR009022; EFG_III_V.
DR  InterPro; IPR005517; EFG_IV.
DR  InterPro; IPR004161; EFTU_D2.
DR  InterPro; IPR005225; Small_GTP.
DR  InterPro; IPR009000; Translat_factor.
DR  Pfam; PF00679; EFG_C; 1.
DR  Pfam; PF03764; EFG_IV; 1.
DR  Pfam; PF00009; GTP_EFTU; 1.
DR  Pfam; PF03144; GTP_EFTU_D2; 1.
DR  PRINTS; PR00315; ELONGATNFCT.
DR  TIGRFAMs; TIGR00484; EF-G; 1.
DR  TIGRFAMs; TIGR00231; small_GTP; 1.
DR  PROSITE; PS00301; EFACTOR_GTP; 1.
KW  Elongation factor; Protein biosynthesis; GTP-binding;
KW  Complete proteome.
FT  NP_BIND      17      24      GTP (BY SIMILARITY).
FT  NP_BIND      81      85      GTP (BY SIMILARITY).
FT  NP_BIND     135     138      GTP (BY SIMILARITY).
SQ  SEQUENCE    695 AA;  76821 MW;  171DD1E2E37FCBEA CRC64;

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Query Match          48.3%;  Score 43;  DB 1;  Length 695;
Best Local Similarity 40.0%;  Pred. No. 20;
Matches      6;  Conservative      7;  Mismatches      2;  Indels      0;  Gaps      0;

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QY      1 LQTPQPLLQVMMEPQ 15
      :: |:|::|| :||:
Db      399 MEFPEPVIQVAIEPK 413

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Search completed: August 24, 2004, 15:43:23
Job time : 10.1343 secs